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92044

From: Sent: To: Subject: P

Gibbs, Terra Tuesday, April 22, 2003 10:53 AM STIC-Biotech/ChemLib Sequence search request...

Could you please do a regular-search of SEQ ID NO:3 of USSN 09/918026?

Terra Gibbs #79523 AU 1635 Mailbox 11E12 306-322

THANK YOU!

Point of Contact: Beverly Shears Technical Info. Specialist M1 1E05 Tel: 308-4994

Searcher:
Phone:
Location:
Date Picked Up:
Date Completed:
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

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April 28, 2003, 03:25:07; Search time 2934 Seconds (without alignments) 15563.157 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-09-918-026A-3 1569 1 atggagccagggggggcccg......cttggtcctgccatacctag 1569 Title: Perfect score: Sequence:

2054640 seqs, 14551402878 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Searched:

4109280 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

GenEmbl:* Database :

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em_htg_other:* em_vi:* em_htg_hum:* em_htg_mus: em_un:

Pred. No. is the number of results predicted by chance to have a

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score greater than or equal to the score of the result being pand is derived by analysis of the total score distribution.

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Homo sapiens acyl Co-A: cholesterol acyltransferase-2 (ACAT2) mRNA, complete cds. AF099031.2 GI:4878036 RESULT 1
AF099031
LOCUS
DEFINITION VERSION KEYWORDS SOURCE ORGANISM ACCESSION

ALIGNMENTS

Homo sapiens.
Homo sapiens
Homo sapiens
Eukaryotta, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryotta; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1569)
Chang, C.C., Sakashita, N., Ornvold, K., Lee, O., Chang, E.T., Dong, R.,
Lin, S., Lee, C.Y., Strom, S.C., Kashyap, R., Fung, J.J., Farese, R.V. REFERENCE AUTHORS

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), 1999 this sequence version replaced gi:3892234.
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 Patoiseau, J.F., Delhon, A. and Chang, T.Y. 'Ological quantitation and localization of ACAT-1
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Direct Submission
Submitted (20-MAY-1999) Biochemistry, Dartmouth, HB
NH 03755, USA
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/function="esterification of cholesterol"
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                                     Biol. Chem. 275 (36), 28083-28092 (2000)
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Mismatches 0;
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Lee,O., Farese,R.V. Jr. and Chang
Human ACAT-2 nucleotide sequence
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/db_xref="taxon:9606"
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/product="acyl coenzyme A:cholesterol acyltransferase 2"
/product="acyl coenzyme A:cholesterol acyltransferase 2"
/product=1,146=34063999.1"
/db_xref="GI:3746539"
/translation="MepGGARLRLORTEGLGGERERQPCGDGNTETHRAPDLVOWTRH
MEAVWAQLLEGOAQOGLRELLDRAMREAIOSYPSOMPRELPPPPPEGSISRYQDESSIGNER
VFIIRKSLLDELMEYQHFRITYHMFIAGLCVFIISTLAIDFIDEGRLLLEFDLLIFSF
GQLDALAYWWPMFLSTLYAPYGALELMARGYWTOATGLGALLAAHAVYLCALDFU
VAUBHOPPASRCVULYEQVRENKSYSFLEARVPGTLRARRGBGIQAPSFSSYLYFLF
CPTLIYRETYPRTPYVRMYVAKNFQALGCVLYACFILGRLCVPVFANMSREPSTR
ALVLSILHATPRETFYPTIFFTHGWLNARFAEMIRFGEDRHYRDWNNSTSFSNYYR
TWNVVVHDWLXSYVYQDGLRLLGARARGVAMLGVFLVSAVAHEYIFCFVLGFFYPWL
IIEFVIGGMINRWHUDQRTGPAMNVLWWTMLELGGGLQVSLYCOEWYARRRCFDLDGAT
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srase 2 mRNA,
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Oelkers, P., Behari, A., Cromley, D., Billheimer, J.T. and Sturley, S.I. Characterization of two human genes encoding acyl coenzyme A. scholesterol acyltransferase-related enzymes J. Biol. Chem. 273 (41), 26765-26771 (1998)
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                                        CTGTTTCTAGGCCAGGGAATCCAGGTCAGCCTGTACTGCCAGGAGTGGTACGCACGGCGG
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Lkers,P., Cromley,D., Behari,A., Billheimer,J.T. and
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Pred. No. 8.9e-303;
); Mismatches 3;
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Direct Submission
Submitted (13-APR-1998) Human Nutrition,
W. 168th Street, New York, NY 10032, USA
Location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="12"
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                                                     CGCACCATCTACCACATGTTCATCGCTGGCCTGTGTCTTCATCATCACCACCTGGCC 420
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Cercopithecus aethiops
Eukaryota; Metazoa; Chordata; Craniata; Vèrtebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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Anderson, R.A., Joyce, C., Davis, M., Reagan, J.W., Clark, M., Shelness, G.S. and Rudel, L.L.
Identification of a form of acyl-CoA:cholesterol acyltransferase specific to liver and intestine in nonhuman primates
J. Biol. Chem. 273 (41), 26747-26754 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              edicine, Wake Forest University
Boulevard, Winston-Salem, NC
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                                                                              GTAGCCATGCTGGTGTTTCCTGGTCTCCGCAGTGGCCCATGAGTATATCTTCTGCTTC
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Anderson, R.A., Joyce, C., Davis, M., Reagan, J.W., Clark, M.
Shelness, G. and Rudel, L.L.
Direct Submission
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/note="liver and intestine specific expression"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Cercopithecus aethiops'
/db_xref="taxon:9534"
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/gene="ACAT2"
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/LTAINSTACTION="MEPGGGRILD.CRTEGPGGEREHOPCROGNTETHRAPDL.VKWHRN
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VFITRKSLLDELMEVQHFRIYMHRTGLCVFITSTLALIPPDGGGLLEFFDSLGKO
VFITRKSLLALVTWVPWELSTLLAPYQALRLWARPGARGTWTLGAGLGGGLGALAAUVLCA
PVHVAVEHOLPPASRCVLVPEQVRFLMKSYSFLREAVPGTLRARRGEGIQAPSFSSY
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FSTRALVLSILHATLPGIPMLLIFFAFLHCWLNAPABMLRGGDREYRDWNNSYSF
NYYRTWNYVHDWILSYYVQDGLWLLGAQARGVAMLGOFLVGAHEX ICRTLGFF
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Pred. No. 9.9e-282;
0; Mismatches 55;
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                                     /protein_id="AAC62929.
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1933 bp mRNA linear ROD 12-JUN-2002 for AcylCoA:Cholesterol Acyltransferase 2, :
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostómi;
Mammalia; Eutheria; Rodentía; Sciurognathi; Muridae; Murinae;
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                          TGCCCAACACTCATCTACAGGGAGACTTACCCTAGGACGCCCTATGTCAGGTGGAATTAT
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Rattus norvegicus mRNA fc
complete cds.
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	FERENCE AUTHORS TITLE JOURNAL SOURC CDS SOURC SE COUNT IGIN		34	88	148	208		328	388	4 4		568	5/4

Katsunori,M., Takeshi,O. and Yukio,F. Cloning and sequence of rat intestinal ACAT2 Unpublished

house mouse. Mus musculus Eukaryota; Meta; Mammalia; Euthe; E 1 (bases 1 to; S strausberg, R. Direct Submission L Submitted (18-Manna) Gene Collection Institute, 31 CG	en, land noole Gen Cen Cen anada	Sen Lee, Victor Ling, Carrie Mather Ness, Pawan Pandoh, Anna-Liisa Pral Schelin, Duane Smailus, Michael Smil Michael Thorne, Miranada Tsai, Nate George Yang, Scott Zuyderduyn, Marc Clone distribution: MGC clone distribution: MGC clone distributions Through the I.M.A.G.E. Consortium/Series: IRAK Plates: 57 Row: f Colur This clone was selected for full le passed the following selection crit	rce .	CDS 60. 1637 /codon_start=1 /product="Similar to sterol O-acyltransfelase 24 /protein_id="AaH25931.1" /db_xref="G1:19684142" /translation="MOPKVPQLRRREGIGEBGEKGARGGEGNARTHGTPDL/OWTR EAVKTOFLEQARELLELIDRALWEANGAPKQDRPLPSÄAFDSTÄKROELHPGKR FITRKSLIDELMEVOHFRITYHMFIAGLCVLIISTLAIDFIDEGRLNLEFDLLIFS OLPLALMTWVPMFLSTLUPYQTLMIWARPRAGGAMMGASIGGCNLAAHAVULCV VHVSVRHELPPASREVIVLEGOVRLLMKSYSFLRETVGIFGCKGKGISPPSTSS FLFCPPLIYRETYPRTPSIRMYVARNFRQVLGCLLYACFILGREGCVPFRSDSS	STRALLISTIHATGPGTFMILLIFFAFUHGWLNAFAEWIRFGDRMFYRDWWNGTSF YYFTWNVVYDMILYSYYQDGLWILGRRARGVAMLGVFLVSAVVHEYIFCFVLGFF VMLMLFLVFGGLLNFTWNDRHTGPAWNILMWTFLFMGGGIQVSLYCQEWYARRHCDF QTTFWGMVTPRSWSCHP" QUETUN QUETUN 71.1%; SCOTE 1115; DB 10; Length 2170; BEST LOCAL Similarity 83.3%; Pred. No. 6.5e-213; Matches 1297; Conservative 0; Mismatches 245; Indels 15; Gaps	28 CTGCAGAGGACAGAAGGCTGGAGGGGGGGGGGGCCCAACCCTGTGGAGATGC 11
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TGGGCTGC TGGGCTGT	CTCCGCAG GTCTGCGG	CATGCTGATAC 	CGGCCCGC	CAGCCTG1	CAGCCTAI	CTGGGGGC 	AF078751 Akoact-2) mRNA, complete AF078751 GI:3746693 AND STAIL GI:3746693 Mus musculus. Mus musculus. Mus musculus. Bukaryota: Metazoa; Chorr Mammalia: Eutheria; Rodes Lases, S., Novak, S., Zhen Welch, C.B., Lusis, A.J.; Melch, C.B., Melch, M
ATCAGGA ATCAAGA	rccregr rccregr	CCGTCAT	AGCGCAC GGCACAC	ATCCAGGTCAGCCT	TCCAGGT	CAACTTT	AF078751 (Acact-2) mRNA, can be many many musculus acyl AF078751.1 GI:37 Mus musculus Mus musculus Mus musculus Bukaryota; Metazo Manmalia; Eutherii Losses 1 to 16 Cases, S., Novak, S. Welch, C.B., Lusis Welch, C.B., Lusis Welch, C.B., Lusis ACAT-2, a second Its cloning, expr. 9756919 10. Biol. Chem. 27 9844591 10. Biol. Chem. 27 9756919 10. Sobilistion Submitted (16-JUL Francisco, CA 941 1. 1607 // Office 184 // Codouct // Product // Product // Protein // Protein // Chramsla
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		Mus sp. peritoneal macrophages. Mus sp. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleost		SOS
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		GGRGIGTICCTGGTCTCCGCAGTGGCCCATGAGIAIATCTTCTGCTTCGTCTGGGGTTC 1332;	1273	da .
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		ACGICCITCICCAACTACCGCACTIGGAACGIGGIGGICCATGACTGGCTGTACAGC 1212.	1153	QY Db
		GCCTTTGCCGAGATGCTACGATTTGGAGACAGGATGTTCTACCGGGACTGGTGGAACTCA 1152 	1093	Qy Up
		TIGCCAGGCAICTICAIGCTGCTGCTCATCTITGCCTICCTCCAITGCTGGCTCAAC 1092	1033	QY Db
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Sciurognathi; Muridae; Murinae; Musi
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
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Uelmen, P. J., Oka, K., Sullivan, M., Chang, C.C., Chang, T.Y., and
1176 AGGAGCCCTTCAGTGCTCGTGTCCTGGTCTGTGTGTTTAACTCCATCTTGCCAGGTG 1235
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acyl-coenzyme A:cholesterol acyltransferase.
Mus musculus cDNA to mRNA.
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RALDA SAPPEGGENETESROSLDELEFUDHTRTYHWFTALLLIEVEVSTIVUVD TDEGRLVLE
RALDA VARGKRPTVTWTWMAARLESTLSIPYEFPGRAAHGYSKSSHDLTYSLVHGLLEV
VPOLGVLGFVPTYVVLAYTLPPASRFILILEQIRLIMKAHSFVRENIPRVLNAAKERS
SAPDLFYVVUQYLYFLAPATLIYRONYPRTPYTWRGVVAMQELOVGVCGLEYYYYIFBRL
CAPLERNIKOBPFSARVLVLCVFNSILDFGVILILESFFAFHGWLNAFABHLRFGDRM
FYKDWWNSTSYSNYYTWWVVHDWLYYYYKOLLWFFSKRRSAAMLAVFALSAVVH
SQBMYAROLGYFFYDLYFFFFFFTHGWLWASLFLGYGLILGFY
SQBMYAROHGHKNPTELDXVRPRTPTTRYNSKRPIWNIWWASLFLGYGLILGFY
6689 C 66689 G 666 L
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protein_ad-"AAB36050.1"
/db_xref="GI:478336"
/translation-"MSLRNRLSKSGENPEQDEAQKNFMDTYRNGHITMKQLIAKKRLL
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              /note="This sequence comes from Fig.
 A:cholesterol
/gene="acyl-coenzyme
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AAEAEELKPLFMKEVGCHFDDFVTNLIEKSASLDNGGCALTTFSILEEMKKNHRAKDL
RAPPEQGKIFISRQSLLDELFEVDHIRIIYHMFIALLILFVLSTIVVDYIDEGRLVLE
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CAPLERNIKQEPFSARVLYLCVFNSTLPGYLILELSFFAFLHCWLNAFAEMLRFGDRA
KYDWWARTSYSKNYYTEWRYVYHUMYTYYYYKKDLLWFFSKRFKSAAMLAVFALSAVVH
EYALAICLSYFYPLYLEVLFWFFRENGARNFIVNDSRKRPIWNIMWASLFLGYGLILCFY
SQEWYARQHCPLKNPFFLDYVRPRTWTCRYYF"
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VFQLGVLGFVPTYVVLAYTLPPASRFILILEQIRLIMKAHSFVRENIPRVLNAAKEKS
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                                                                                                   /note="amino acid feature: N-glycosylation site, aa 399;
                                                                                                                                             /product="acyl-coenzyme A: cholesterol acyltransferase"
/protein_id="AAC42075.1"
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Matches 769; Conservative
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Takahashi,K., Shichiri,M. and Horiuchi,S.
Molecular cloning, functional expression and tissue distribution of
rat acyl-coenzyme A:cholesterol acyltransferase
Biochim Biophys. Acta 1391 (2), 193-203 (1998)
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                    1840 AGGAGCCCTTCAGTGCTCGTGTCCTGGTCTGTGTTTAACTCCATCTTGCCAGGTG 1899
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GGACGCCCTATGTCAGGTGGAATTATGTGGCCAAGAACTTTGCCCAGGCCCTGGGATGTG 922
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                          TCTTCATGCTGCTCATCTTCTTTGCCTTCCTCCATTGCTGGCTCAACGCCTTTGCGG
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                                                                    TGCTCTATGCCTGCTTCATCCTGGGCCGCCTCTGTGTTCCTGTCTTTGCCAACATGAGCC
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Matsuda,H., Hakamata,H., Kawasaki,T.,
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Direct Submission
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53

Apr

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RLVLEFSLLATARGOPPIVIWWAMPLSTLAIPYFLFORWHRITSLEDGE
GAFELVPOLGILGFTPTYVLAYTLPPASRFILLIEQIRLVWKAHSYSKSSHPLISLLA
GAFELVPOLGILGFTPTYVLAYTLPPASRFILLIEQIRLVWKAHSYVREWYPRVLSA
AKRSSTVPVPTVNOYLYFLFAPTLIYNESYPFTPTVRWGYVAMOFLOYGCLFYVYY
IFERCAPLERNIKOBFFSARVLVCVFNSILLPGVLMLFLSFFAFHCWLNAFAEMLR
FGDRMFYKDWWNSTSYSNYYRTWNVVVHDMLYYYVYKDLLWFFSKRFRPAMMLAVFAL
SAVYHRENARQCPLKNPFLDYFLEWFGMARRITVNDSRKRPVWNINWRASLFLGHGY
ILCFYSOGWARARQCPLKNPFLDYVRPRTWTCRYVF"
456 C 409 9 504 t
                                                                                                                                                                                                                                   /translation-"MVGEETSLRNRLSRSAENPEQDEAQKNLLDTHRNCHITMKQLIA
KKRQLAAEAEELKPLFLKEVGCHFDDFVTNLIDKSASLDNGGCALTTFSILEEMKNNH
RAKDLRAPPEQGKIFISRRSLLDELFEVDHIRTIYHMFIALLIIFILSTLVVDYIDEG
 University School
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of Medicine, Department of Blochemistry; Honjo 2-2-1, Kumamoto,
Kumamoto 860-0811, Japan (E-mail:horiuchi@gpo.kumamoto-u.ac.jp,
Tel:81-96-373-5068, Fax:81-96-364-6940)
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                                                                                                                                                                                         /product="acyl-coenzyme A:cholesterol
/protein_id="BAA25372.1"
/db_xref="G1:3036905"
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 412.2; DB 10;
Pred. No. 2.6e-72;
); Mismatches 513;
                                                                                    /organism="Rattus norvegicus"
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                                                                                                                                           /tissue_type="adrenal grand"
                                                                                                            /db_xref="taxon:10116"
/sex="male"
                                                          Location/Qualifiers
                                                                                                   /strain="Wistar"
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(bases 1 to 1673)

Anderson, R.A., Joyce, C., Davis, M., Reagan, J...

Shelness, G.S. and Rudel, L.L.

Identification of a form of acyl-CoA:cholesterol adyltransferase specific to liver and intestine in nonhuman primates

Specific to liver and intestine in nonhuman primates

Them. 273 (41), 26747-26754 (1998)
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GGACGCCCTATGTCAGGTGGAATTATGTGGCCAAGAACTTTGCCCAGGCCCTGGGATGTG 922
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                                                         1GCTCTATGCCTGCTTCATCCTGGGCCGCCTCTGTGTTCCTGTCTTTGCCAACATGAGCC
                                                                      AGATGCTACGATTTGGAGACAGGATGTTCTACCGGGACTGGTGGAACTCAACGTCCTTCT
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Catarrhini, Cercopithecidae;
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates;
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Anderson, R.A., Joyce, C., and Rudel, L.L.
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SKNNRRAKDLRAPPEQGKIFTARRSLLDELLEVDHIFTIYHMPIALLIETLGTLVVD
YIDEGRIVLEFSELLSZAFGKFPTVVWTWMINFLSTFBSVPYFLFQRMANGYSKSSHPLI
NSLFHGFLFWVFQIGLIGFGPTYVVLAYTLPPASRFIIFFGQIFFVWKAHSFVRENVP
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AEMLERGDRÆFKDWWNSTSYSNYYRWNVVVHDWLYYYAYKRFEKPRFKSAAML
AVAVSAVVHEYALAVCLFFYPYVLYFFFFFYPTPLLYRPFGMAFNFIVNDSRKKPIWNVMMTSLF
LGNGYLLCFYSQEWARQHCFLKNPFFLDYVRPRSWTCRYVF"
359 c 359 g 550 t
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/product="acy1_CoA:cholesterol acy1transferase 1"
/protein_id="AAC65930.1"
/db_xref="GI:3582757"
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Pred. No. 6e-72
0; Mismatches
                          Center
                                                                       /organism="Cercopithecus
/db_xref="taxon:9534"
/tissue_type="adrenal"
              Internal
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/function="catalyzes
                                                 Location/Qualifiers
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Direct Submission
Submitted (11-MAR-1998)
School of Medicine, Medi
27157, USA
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Molecular cloning and functional expression of human acyl-coenzyme A:cholesterol acyltransferase cDNA in mutant Chinese hamster ovary
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Catarrhini; Hominidae;
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Mammalia; Eutheria; Primates;
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RVLNSAKEKSSTVPIPTVNQYLYFLFAPTLIYRDSYPRNPTVRWGYVAMKFAQVFGCF
FYVYYIFERLCAPLFRNIKQEPFSARVLVLCVFNSILPGVLILFLTFFAFLHCWLNAF
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AVFAVSAVVHEYALAVCLSFFYPVLFVLFMFFGMAFNFIVNDSRKKPIWNVLMWTSLF
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/protein_id="AAC37532.2"
/db_xref="GI:4878022"
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                                              Submitted (02-NOV-1993) Biochemistry Dept, Dartmouth Medical
                                                                                                      Submitted (20-MAY-1999) Biochemistry Dept, Dartmouth Medical School, Hanover, NH 03755, USA Sequence update by submitter on May 20, 1999 this sequence version replaced gi:409203. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATCCCTGGGGAAACAGAAAGTTTCATCATCGCAAGTCCCTGCTTGATGAGCTGATGG
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="THP-1 (Phorbol ester ac/cell_type="macrophage"
1397. .3049
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Pred. No. 2.4e-71;
0; Mismatches 508
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                                                          School, Hanover, NH 03755, USA
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           2 (bases 1 to 4011)
Chang, C.C. and Chang, T.Y.
Direct Submission
                                                                      3 (bases 1 to 4011)
Chang, C.C. and Chang, T.Y.
Direct Submission
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Sciurognathi, Muridae, Cricetinae;
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                                                                                                                                                                               GTCAACCAGTATTTGTACTTCTTATTTGCTCCTTATCTACGGGGGGCTATCGC 2335
                                                                                                                                                                                                                                                                                          AGGAATCCCACTGTAAGATGGGGTTATGTCGCTATGAAGTTTGCACAGGTCTTTGGTTGC 2395
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Cricetulus griseus
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
Cricetulus.
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          Cao,G., Goldstein,J.L. and Brown,M.S.
Complementation of mutation in acyl-CoA:cholesterol acyltransferase (ACAT) fails to restore sterol regulation in ACAT-defective sterol-resistant hamster cells
96278939
                                                                                                                                                                                                                                                                                                            /translation="MYGEEKMSLRNRLSKSGENPEODEAQRSVSDTQSNGRITMKQLI
AKKRQLAAEAEELKPLFLKEVGCHFDDFVTNLIEKSASLDNGGCALTTFSILEEMKNN
HRAKDLRAFPEKGKIFISRRSLLDELFEVDHIRTIYHMFIGLLILFILSTLVVDYIDE
                                                                                                                                                                                                                                                                                                                                                   GRLVLEFNLLGYAFGKLPTVIWTWWAMFLSTLSIPYFLEQRWAHGYSKTSHPLIYSLS
HGFFELVFQLGILGFVPTYVVLAYTLPPASRFTVILEQIRWMKAHEFVRENVPRVLN
AAKEKSSTVOVPTVNOYLYFPLPAPTITYBDSYPRTPTVRWGYVAVQFLQVFGCLFYVY
YIFERLCAPLFRNIQQEPSARVLVLCVFNSTLDGVLMLFLFFFFHJHGWLANFAEML
RFGDRWFYKDWWNSTSYSNYYFTWNVVVHDWLYYYAYKDLLWFFSKRFKSAAMLAVFA
ISAVYHEYALANCLSYFYPVLFVLFWFGMARNFTVNDSKKRFIWNIMVWASLFLGHG
3024
                                                                                                               Cao,G., Brown,M.S. and Goldstein,J.L.
Direct Submission
Submitted (26-JAN-1996) Guoqing Cao, Molecular Genetics, University
off Texas Southwestern, 5323 Harry Hines Blvd., Dallas, TX 75235,
USA
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0; Mismatches 516;
                                                                                                                                                                                                       /organism="Cricetulus griseus"
/db_xref="taxon:10029"
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Pred. No. 3.6e-71
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674 c 651 g 979
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/db_xref="GI:1408466"
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1. .3024
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AF354622 1528 bp mRNA linear PRI 17-APR-2002 Gorilla gorilla cholesterol acyltransferase 1 (ACAT1) mRNA, partial
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Catarrhini; Hominidae; Gorilla.
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Mammalia; Eutheria; Primates;
1 (bases 1 to 1528)
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AF354622.1 GI:18028941
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HFDDFVTNLIEKSASLDNGGCALTTFSVLEGEKNNHRAKDLRAPPEQGKIFIARRSLL
                                                                                                                                                                                                                                                                                              DELLEVDHIRTIYHMFIALLILFILSTLVVDYIDEGRLVLEFSLLSYAFGKFFTVVWT
WWIMPLSTSYPYRELDQHWARGYSKSBHDLIRSLHGFLFERELSTSTSTSTYVULA
YTLPPASRFIIIFOLFVWARHSFYRENDFRVLGAREKSSTVPIPPUVQYLYFLFA
PTLIYRDSYPRNPTVRWGYVAMKFAQVFGCFFYVYIFFERLAPLERLAPFKNUNYLFFERN
VLOVFVNILLBOYLLLETFFFAELHGWARARFREGDRAPKTKDWNSTSYSYYYTY
WNVVVHDMLYYYARANDEWFFSKFRSGAAMANFASGANAHSYAULASFFPYDLFY
LEMFFGMAFNFINDSRKKPIMNVLAMTSLFIGNGVLLCFYSGEWYARQHCPLKNPTF
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Park, PA 16802, USA
        paleontological
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         constraints on
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                                                              2 (bases 1 to 1528)
Hedges,S.B.
Direct Submission
Submitted (27-FEB-2001) Department of Biology,
State University, 208 Mueller Lab, University in Location/Qualifiers
                                                                                                                                                                      cells
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 405.8; DB 9;
Pred. No. 5e-71;
0; Mismatches 487;
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/db_xref="taxon:9593"
/cell_type="cultured fibroblast
<1. .>1528
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                         J. Hered. 92 (6), 469-474 (2001) 21945518
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EC028940.1 GI:20809439
MCC
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                                      ACGTGCGTACTAAT-TCAGCTAAGGAGAAATCAAGCACTGTTCCAATACCTACA
                                                                                                                                                                               GECAACCAGTATTTGTACTTCTTATTTGCTCCTACCCTTATCTACGTGACAGCTATCCC
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                                                                                                                                             G-----CTACCTCTACTTCCTCTTCTGCCCAACACTCATCTACAGGGAGAGTTACCĆT
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Mammalla; Eutheria; Primates;
1 (bases 1 to 3407)
Strausberg, R.
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| ACATTTT 1527
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JOURNAL	Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Traffitted 21 Control Date Property 11802	Qy	527
	institute, of tenter Dilve, know liAus, Bethesda, MD 20892-2590, USA	qq	644
REMARK COMMENT	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk	QY	, 587
	Email: cgapos remail.nin.gov Tissue Procurement: ATCC	qa	704
	CDNA Library Freparation: Lite Technologies, Inc. CDNA Library Arrayed by: ThA I.M.A.GE. Consortium (LLNL) DNA Sequencing by: Raylor College of Medicing Human Genema	Qy	647
		qa	764
	Web site: http://www.bgc.bcm.tmc.edu/cdna/ Contact: amm@hcm tmc edu	ΟŶ	689
	Gurantne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S. Martin, P.G. Marny, D.M.	qa	824
	ds, S., Gibbs, R.A.	δλ	749
	Clone distribution: MGC clone distribution information can be found	qq	884
	Series: IRAK Plate: Consocramy Law are incled, image law as selected for il Column; 23 This clone was selected for full length securencing because it	ΟY	808
	passed the following selection criteria: Similarity but not identity to protein	qq	943
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Chang, T. Y. and Chang, C.C.Y.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Description	Human ACAT Related	Human acyl CoA:cho	Mouse acyl CoA:cho	Human acylcoenzyme	Acetyl coenzyme A:	Human acylcoenzyme	Human acyl-coenzym	Acylcoenzyme A:cho	Drosophila melanog
SUMMARIES		AAZ57360	AAZ57359	AAV01534	AAQ63212	AAV01536	AAT96368	AAV01545	ABL13759
DB	21	21	21	13	15	13	19	19	23
a Query e Match Length DB	2040	1509	1607	1082	4011	3649	3650	455	1885
% Query Match	99.7				26.0				
Score	1564.2	1425.8	1112.4	645	407.2	404	394.6	191.8	172
Result No.	-	7	3	4	D.	ø	7	80	ō

	10	172	11.0	2657	23	ABL15694 ABL13758	Drosophila melanog
	12			966	15	-	Acetyl coenzyme A:
	13	95		983	19	AAV01539	Human acylcoenzyme
υ	14	95		993	22	ABA06413	Human cDNA SEQ ID
	15	95		1521	19	AAV01533	Human acylcoenzyme
	16	95		1895	21	AAA88842	ď
	17	95		1895	21	AAZ45383	DNA encoding a pro
	18	95		1976	21	AAA76169	Human ACAT Related
	19	ω.		542	22	AAS27552	cDNA encoding nove
	20	ď.		774	22	AAS27244	cDNA encoding nove
	21	88.2	5.6	447	21	AAC28517	Human secreted pro
	22	\vdash	•	452	24	ABL81686	Human ovarian canc
	23	Н		1650	21	AAZ49452	Mouse Diacylglycer
	24	80		1122	20	AAX30335	DNA encoding a hum
	25	9		1766	21	AAA88846	Rat acyl CoA:chole
	56	9		1766	21	AAZ45385	Acyl-CoA:cholester
	27	79.8	5.1	1766.	22	AAS01105	Rat sterol acyltra
	28	0		1559	21	AAA48935	
	58	9		978	21	AAA48934	Corn diacylglycerb
	30	9		1281	21	AAA48933	Corn diacylglycero,
	31	65		901	21	AAA48936	Corn diacylglycero
	32	64.8	4.1	1587	21	AAA48938	Rice diacylglycero
	33	9.09		5574	24	AAS63338	Chemically pretrea
	34	0		1975	21	AAA48942	Wheat diacylglycer
	35	09		9	24	ABN36849	Human spliced tran
	36	59		1942	21	AAA48939	Soybean diacylglyc
	37	2		4170	22	AAK69416	Human 1mmune/haema
	38	S		519	21	AAA88843	M. alpina acyl CoA
	39	55.4		519	21	AAZ45380	굯
	40	5		519	22	AAS01319	Mortierella alpina
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	42	20		1888	21	AAA48932	Ø
	43	20		1904	21	AAA51482	g G
	44	20	•	1942	21	AAA88835	Ø
	45	20		1942	21	AA245371	ž
						ALIGNMENTS	

AAA76170 standard; DNA; 2040 BP 14-DEC-2000 (first entry) AAA76170; AAA76170

Human ACAT Related Gene Product 2 ARGP2 coding sequence.

Human; ACAT Related Gene Product 2; ARGP2; enzyme; acyl Coenzyme A-cholesterol acyltransferase 1; ACAT1; ACAT2; sterol esterification; lipid homeostasis; diacylglycerol acyltransferase;

Homo sapiens

Location/Qualifiers 52.1620 /*tag= a /product= "Human ARGP2" 98US-0165042 01-OCT-1998; US6100077-A. 08-AUG-2000. Key

(UYCO) UNIV COLUMBIA NEW YORK. 98US-0165042. 01-OCT-1998;

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                                                                                                   The enzyme acyl Coenzyme A-cholesterol acyltransferase 1 (ACATI) mediates sterol esterification, an important component of intracellular lipid homeostasis. The present sequence is the coding sequence of human ACAT Related Gene Product 2 (ARGP2/ ACAT2). The enzyme encoded by the present sequence is a diacylgy/vectol acyltransferase (DGAT). ARGP2 seterifies cholesterol. Also, the activity of ARGP2 is relatively resistant to histidine active site modifier. ARGP2 is therefore a tissue specific
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                                           New nucleic acid encoding a human diacylglycerol acyltransferase, useful for treating hyperlipidemia, atherosclerosis, heart disease, other diseases associated with an imbalance of triglyceride levels
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Pred. No. 0;
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ilarity 99.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes the human acyl CoA:cholesterol
acyltransferase designated ACAT-2. ACAT-2 polypeptides can be
acyltransferase designated ACAT-2. ACAT-2 polypeptides can be
administered therapeutically, especially by expressing encoding
polynucleotides, to treat individuals in need of ACAT-2 polypeptide.
They may especially be administered to treat disease conditions
associated with elevated cholesterol ester levels e.g.
hypertrolesterolaemia or hyperlipidaemia (including
hypertrolesterolaemia) and paperlipidaemia (including
hypertrolesterolaemia) and paperlipidaemia (including
hypertrolesterolaemia) and paperlipidaemia (including
hypertrolesterolaemia) and substrates. The polypeptides can also
be used to dispose diseases related to polypeptide expression or
activity, by analysing for polypeptide presence or amount in a sample.
They are useful to screen for compounds inhibiting or activating the
polypeptide, which can be included in pharmaceutical compositions and
administered therapeutically to treat conditions associated with ACAT-2;
inhibitory agents can especially be used to inhibit ACAT-2 activity,
this to man and the paperlially agents which selectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel polypeptide, useful to treat conditions associated with elevated cholesterol ester levels e.g. hypercholesterolemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGACCCGACACGAGGCTGTGAAGGCACAATTGCTGGAGCAAGCGCAGGACAACTG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TGGACCCGACACATGGAGGCTGTGAAGGCACAATTGCTGGAGCAAGCGCAGGGACAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21; Length 1509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90;
antilipaemic; hypercholesterolaemia; hypertriglyceridaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1509 BP; 260 A; 457 C; 439 G; 351 T; 2 other;
                                                                                                                                                     /transl_except= (pos:571..573,aa:Xaa)
/note= "Xaa is unspecified"
                                                                                                                                                                                                                                                                                                                                                                                               SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1425.8;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               Erickson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inhibit ACAT-2 and not prior art ACAT-1.
                                                                                   ocation/Qualifiers ...1509
                                                                                                                   /*tag= a
/product= "ACAT-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
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95.6%;
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99US-0328857
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Matches 1500; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57pp;
                                                                                                                                                                                                                                                                                                                                                          (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                             Farese RV,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; Page 52;
              hyperlipidaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAY67953
                                                   sapiens
                                                                                                                                                                                                     W09967368-A1
                                                                                                                                                                                                                                                                      16-JUN-1999;
                                                                                                                                                                                                                                                                                                                          38-JUN-1999;
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                                                                                                                                                                                  polypeptide, useful to treat conditions associated with elevated sterol ester levels e.g. hypercholesterolemia
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                                                                                                            AACTTCATGATGCATGACCAGCGCACCGGCCATGGAACGTGCTGATGTGGACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; acyl CoA:cholesterol acyltransferase; ACAT-2; diagnosis; antilipaemic; hypercholesterolaemia; hypertriglyceridaemia; hyperlipidaemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acyltransferase 2 encoding
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30..1607
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/product= "ACAT-2"
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P-PSDB; AAY67952.
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08-JUN-1999;
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polypeptide, which can be included in pharmaceutical compositions and administerate therapeutically to treat conditions associated with ACAT-2; inhibitory agents can especially be used to inhibit ACAT-2 activity, especially therapeutically, and especially agents which selectively inhibit ACAT-2 and not prior art ACAT-1.
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                                                                                                                 21; Length 1607;
                                                                                                              Score 1112.4; DB 21; Lengt
Pred. No. 3.7e-267;
0; Mismatches 247; Indels
                                                                                        Sequence 1607 BP; 299 A; 466 C; 456 G; 385 T; 1 other;
                                                                                                              Query Match 70.9%;
Best Local Similarity 83.2%;
Matches 1295; Conservative
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                                       GGGCCAGGCATCTTCATGCTGCTCCTCATCTTCTTCGCCTTCCTGCAGCCTGCTGCTCACCTAAC
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                                                                                                                                                                                                                                                                                                           This isolated nucleic acid molecule encodes human acylcoenzyme A:cholesterol acyltransferase III (see AAW43407), or ACAT related gene product 2 (ARGP-2), whose expression appears to be restricted to the foetal liver, suggesting it to have a role in lipid metabolism during development. It was identified following database searching for human ACAT-related sequences and use of PCR and RACE to obtain full-length sequences. An isolated nucleic acid (see AAV01533) for human ARGP-1 (see AAW43406) was also identified. Also claimed are host vector systems for production of ARGP-1 and ARGP-1 con-human mammals. ARGP-1 and ARGP-1 nucleic acids can be used to treat or diagnose a subject who has an imbalance in sterol levels due to a defect in esterification of sterols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid molecule, or a vector expressing the oligonucleotide, can be used to inhibit wild-type ARGP-1 or ARGP-2. The wild-type enzymes can be used to identify an inhibitor, useful in the treatment of atherosclerosis or hyperlipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGCTGTACAGCTACGTGTATCAGGATGGGCTGCGGCTCCTTGGTGCCCGGGGCCGAGGG
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                                                                                                                                UNA encoding acylcoenzyme A: cholesterol acyltransferase
III - useful to identify inhibitors for treatment of
atherosclerosis or hyperlipidaemia
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Pred. No. 9.4e-151;
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Conservative
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This sequence is a human ACAT cDNA sequence designated K1.
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                                                                                                                                                                                                                                                                                                                                                                                          Acetyl CoA: cholesterol acetyltransferas
             CTGTTTCTAGGCCAGGGAATCCAGGTCAGCCTGTACTGCCAGGAGTGGTACGCACGGCGG
                                                                        544 CTGTTTCTAGGCCAGGGAATCCAGGTCAGCCTGTACTGCCAGGAGTGGTACGCACGGCGG
                                                          CACTGCCCCTTACCCCAGGCAACTTTCTGGGGGCTGGTGACACCTCGATCTTGGTCCTGC
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                                                                                                                                                                                                                                                                             coenzyme A; cholesterol acetyltransferase; ACAT; disease;
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/*tag= b
7.0tc= "Putative polyadenylation signal."
3962..3967
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                                                                                                                                                                                                                                                                                      diagnosis, detection; screening; treatment; prophylaxis; hypercholesterolaemia; atherosclerosis; antisense; probe; identification; ss.
                                                                                                                                                                                                                                                      Acetyl coenzyme A: cholesterol acetyltransferase (ACAT).
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/note= "Putative polyadenylation signal.
                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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P-PSDB; AAR53079.
                                                                                                     CATACCTAG 1569
                                                                                                                  CATACCTAG
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                                            Length 4011;
                                                                                                                                                                                                                                                                                                                            Score 407.2; DB 15; Length
Pred. No. 2.8e-91;
0; Mismatches 508; Indels
Sequence 4011 BP; 1056 A; 793 C; 839 G; 1323 T; 0 other;
                                            26.0%;
59.0%;
                                            Query Match 26.0
Best Local Similarity 59.0
Matches 768; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acylcoenzyme A:cholesterol acyltransferase; ACAT I; ACAT related gene product 1; ARGP-1; ARP-2; sterol esterification; Inhibitor; atherosclerosis; hyperlipidaemia; human; ss.
2756 GCTGTATCTGCTGTAGTACACGAATATGCCTTGGCTGTTTGCTTGAGCTTTTCTATCCC
                                                                                                       GTCATGCTGATACTCTTCCTTGTCATTGGAGGAATGTTGAACTTCATGATGCATGACCAG
                                                                                                                          1462 CAGGTCAGCCTGTACTGCCAGGAGTGGTACGCACGGCGCCACTGCCCCTTACCCCAGGCA
                                                                                                                                                                                                                                              1936 TTACTCTGCTTTTATTCTCAAGAATGGTATGCACGTCGGCACTGTCCTGAAAAATCCC
                                           CTGGTCTCCGCAGTGGCCCATGAGTATATCTTCTGCTTCGTCCTGGGGTTCTTCTATCCC
                                                                                                                                                                  CGCACCGGCCCGGCATGGAACGTGCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATC
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treatment of
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                                                                                                                                                                                                                                                                                                         DNA encoding acylcoenzyme A: cholesterol
III - useful to identify inhibitors for
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P-PSDB; AAW43409.
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                                                                                  ACGTGCCTCGGGTACTAAAT-TCAGCTAAGGAGAAATCAAGCACTGTTCCAATACCTACA 2275
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                                                                CATCCCTGGGGAAACAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTGATGAGCTGATGG
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 Length 3649;
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Score 404; DB 19;
Pred. No. 1.7e-90;
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Match 25.7%;
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                                                                                                                          1462 CAGGICAGCCIGIACTGCCAGGAGTGGIACGCACGGGGGCACTGCCCCTTACCCCAGGCA 1521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This DNA sequence includes a coding region for human macrophage acyl-coenzyme A:cholesterol acyltransferase I (hACAT) (see AAW38416) It has been used to search for homologous yeast genes (see AAT96369 and AAT96370) and subsequently to identify an additional human isoform (see AAW38421). A novel claimed expression vector (I)
                                             GTCATGCTGATACTCTTCCTTGTCATTGGAGGAATGTTGAACTTCATGATGCATGACCAG
                                                                                                2756 GCTGTATCTGCTGTAGTACACGAATATGCCTTGGCTGTTTGCTTGAGCTTTTTCTATCCC
                                                                GIGCIGITCGIGCICTICAIGITCTITGGAATGGCTITICAACTICATTGTCAATGATAGI
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//transl_except= (pos:2492..2495, aa:Val)
//note= "this codon has an apparent 1 nucleotide insertion, which alters the reading
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                                                                                                                                                                                                                                                                                                                  Acyl-coenzyme A: cholesterol acyltransferase I; ACAT; humasterol; esterification; arteriosclerosis; hyperlipidaemla; antifungal; fungicide; ss.
                                                                                                                                                                                                                                                                                                  Human acyl-coenzyme A:cholesterol acyltransferase I DNA
                                                                                                                                                                              ACTITCIGGGGCTGGTGACACCTCGATCTTGGTCCTGCCAT 1563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 61-63; 111pp; English
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comprises an isolated nucleic acid molecule encoding yeast wild type acyl-coenzyme A:cholesterol acyltransferase I (AREI) (see AAW38417) or 2 (ARE2) (see AAW38418) operatively linked to a promoter. The vector and a claimed host-vector system can be used for the recombinant production of AREI or ARE2. The products can be used to identify novel AREI or ARE2 inhibitors. ARE2 inhibitors can be used to treat arteriosclerosis or hyperlipidaemia, as well as to inhibit fungal growth or to treat fungal invasion (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                            CATCCCTGGGGAAACAGAAAGTTTTCATCATCGCAAGTCCCTGCTTGATGAGCTGATGG 346
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Matches 193; Conserv
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                                                                      Sequence 455
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treatment of
                                                                                                                                                                                                                                                                                                                            CACATTTTTGGATTATGTCCGGCCACGTTCCTGGACTTGTCGT 3038
                                                                                                                                                                                                                                                                                                             1521 AACTITCIGGGGGTGGTGACACCICGAICTIGGICCTGCCAI 1563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acylcoenzyme A:cholesterol acyltransferase; ARGP-1; ACAT related gene product; sterol esterification; Inhibitor; atherosclerosis; hyperlipidaemia; ss.
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inhibitors for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
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1 to identify in}
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P-PSDB; AAW43413.
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                                                                                                                                                                                                                                           1375 AIGTTGAACTTCATGATGCATGACCAGCGCACCGGCCTGGAACGTGCTGATGTGG 1434.
                                                                                                                                                                                                                                                                                                                       ACCATGCTGTTTCTAGGCCAGGGAATCCAGGTCAGCCTGTACTGCCAGGAGTGGTAGGCA 1494
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human
(see
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                and mouse acylcoenzyme A:cholesterol acylclus.com. AAW43406-08), also designated ACAT related gene products (ARGP) and 2. These can be used to identify inhibitors useful in the treatment of atherosclerosis and hyperlipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NO 35759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             developmental biology; cell signalling; insecticid
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  coding
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AAV01533-35)
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0; Mismatches
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11-JUL-2000; 2000US-0614150.
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genes from Drosophila and
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                                                                                                              Gaps
          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                    Length 1885;
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                                                            Sequence 1885 BP; 410 A; 514 C; 504 G; 457 T; 0 other;
                                                                                  Score 172; DB 23;
Pred. No. 8.5e-33;
0; Mismatches 380;
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                                                         Drosophila melanogaster expressed polynucleotide SEQ ID NO 41564.
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                                                                                                               developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 genes from Drosophila and for elucidating cell signalling and cinteractions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the pri specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
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Pred. No. 9.6e-33;
0; Mismatches 380;
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Best Local Similarity 51.9%;
Matches 413; Conservative
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11-JUL-2000; 2000US-0614150
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(first entry)
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                                                                                                                                                pharmaceutical; gene;
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is
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 CCGGGACTGGTGGAACTCAACGTCCTTCTCCAACTACTACCGCACTTGGAACGTGGTGGT
             CCGAGGGTAGCCATGCTGGGTGTTCCTGGTCTCCGCAGTGGCCCATGAGTATATCTT
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                                            CCATGACTGGCTGTACAGCTACGTGTATCAGGATGGGCTGCGGCTCCTTGGTGCCCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NO 35756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ss.
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genes from Drosophila and interactions -
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P-PSDB; ABB69655.
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useful in developmental biology and in circuity of cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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Pred. No. 1.2e-32;
0; Mismatches 380; Indels 3;
                                                                                                                                 Sequence 4260 BP; 1152 A; 961 C; 962 G; 1185 T; 0 other;
                                                                                                                                                         Query Match
Best Local Similarity 51.9%;
Matches 413; Conservative (
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P-PSDB; AAW43412.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 AGGIGCAGCATTTCCGCACCATCTACCACATGTTCATCGCTGGCCTGTGTGTCTTCATCA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 CACCTCCAGAACAAGGAATTTTATTGCAAGGCGCTCTCTTTAGATGAACTGCTTG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The acetyl coenzyme A: cholesterol acetyl-transferase (ACAT) gene sequence enables the screening of human populations for abnormal human ACAT activities for disease diagnosis. It provides information concerning the catalytic mechanism of ACAT and allows the design of drugs serving as specific ACAT inhibitors, desirable for the prevention and/or treatment of human hypercholesterolaemia and human atherosclerosis. It also allows the design of antisense DNAs or RNAs to inhibit ACAT prodction, or probes to identify different forms of human ACAT or ACAT from different animal species This sequence is a human ACAT clone designated CI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         442 CCTGTCTTATGCATTTTGGCAAATTTCCTACCGTTGTTTGGACCTGGTGGATCATGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465 ACTG-ATCTTCAGCTTCGGACAGCTGCCATTGGCGCTGGTGACCTGGGTGCCCATGTTTC
                                                                                                                                                                                                                                                                               ACAT; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acetyl coenzyme A: cholesterol acetyl-transferase and nucleic acid sequence encoding it - used to correct enzyme deficiencies and screen for enzyme inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
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0; Mismatches 324; Indels
                                                                                                                                                                                                                                                                                                      liagnosis; detection; screening; treatment; prophylaxis;
lypercholesterolaemia; atherosclerosis; antisense; probe;
                                                                                                                                                                                                                      Acetyl coenzyme A: cholesterol acetyltransferase (ACAT).
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                                                                                                                                                                                                                                                                            cholesterol acetyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 134.6;
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                                                      AAQ63210 standard; cDNA; 996
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93US-0121057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 53.1
Matches 390; Conservative
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                                                                                                                                                                                                                                                                               coenzyme A;
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10-SEP-1993;
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RESULT 12
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                                                                                                                                                                                                                         622 GAGTICTAGGTTTTGGACCAACATATGTTGTGTTAGCATATCCTGCCACCAGCTTCCCGG ·681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        802 ACCAGRATITGIACTICITATITGCICCTACCTIATCTACCGIGACAGCTATCCCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   862 ATCCCACTGTAAGATGGGGTTATGTTGCTATGAAGTTTGCACAGGTCTTTGGTTGCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human acylcoenzyme A:cholesterol acyltransferase II (ACAT :II) DNA.
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                                                                       562 GITCTCATCCGCTGATCCGTTCTCTTTCCATGGCTTTCTTTTCATGATCTTCCAGATTG
                                                                                                                                                                                                                                                                                                    751 GTGCCTGGGATCCTTCGTGCCAGACGAGGTGAGGGGATCCAGGCC-----CCCAGTTTCT
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                                                                                                                                                      ---TGCGCGCTGCCGGTCCACGTGGCCGTGGAGCATCAGCTCCCGCCGGCCTCCCGTTGT
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584 AGGCGACGGGCTTGGGGCTTTTTAGCCGCCCACGCCGTGGTGCTC
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ACAT related gene product 1; ARGP-1; ARP-2; sterol e
inhibitor; atherosclerosis; hyperlipidaemia; human;
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2000US-241221P
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                                                                                                                                                                                                                                                                     1079 ATTGCTGGCTCAACGCCTTTGCCGAGATGCTACGATTTGGAGACAGGATGTTCTACCGGG 1138
                                                                                                                                                                                                                                                                                                                                                                                                  ACTGGTGGAACTCAACGTCCTTCTCCAACTACCGCACTTGGAACGTGGTGGTCCATG 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1199 ACTGGCTGTACAGCTACGTGTATCAGGATGGGCTGCGGCTCCTTGGTGCCCGGGCCCGAG 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGTAGCCATGCTGGTGTTCCTGGTCTCCGCAGTGGCCCATGAGTATATCTTCTGCT 1318
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                                                                                                                                                                                                                                                                                       182 TCCTGAAGCTGGCGGTCCCCAATCACCTCATCTGGCTCATCTTCTACTGGCTCTTCC 241
                                                                                                                                                                                                                                                                                                                                                                                                                   416 GGATGCCCAGGACAGGGGTGTTCCTGGCCTCGGCTTTCTTCCACGAGTACCTGGTGAGCG 475
                                            This nucleic acid molecule encodes human acylcoenzyme A:cholesterol acyltransferase I (see AAW412), or ACAT II. The invention relates to isolated nucleic acids (see AAV01533-15) coding for human and mouse acylcoenzyme A:cholesterol acyltransferase II and III (see AAW4406-08), also designated ACAT related gene products (ARGP) 1 and 2. These can be used to identify inhibitors useful in the treatment of atherosclerosis and hyperlipidaemia.
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; proliferative disorder; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                   362 AGTGGTGCATCAGACACTTCTACAAGCCCCATGCTTCGAC-----GGGGCAGCAGCAAGT
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9
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                                                                                                                                                                                                      Score 95; DB 19; Length 983;
Pred. No. 1e-13;
0; Mismatches 125; Indels
                                                                                                                                                                        Sequence 983 BP; 193 A; 314 C; 263 G; 213 T; 0 other;
                Disclosure; Page 68; 121pp; English
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Best Local Similarity 58.79
Matches 186; Conservative
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19-MAY-2000;
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Sequence 993 BP; 218 A; 260 C; 328 G; 186 T; 1 other;

is a cDNA of the invention.

SXCC

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Isolated nucleic acid molecule encoding an inflammation-associated polypeptide is used in preventing, treating or ameliorating a medical condition -
                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO: 79; 859pp + Sequence Listing; English.
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                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                        Rosen CA, Barash SC,
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P-PSDB; ABB10191.
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1259 GGGTAGCCATGCTGGTGTTCCTGGTCTCCGCAGTGGCCCATGAGTATATCTTCTGCT 1318
                                                                                        1019 TCCTGCATGCCACGTTGCCAGGCATCTTCATGCTGCTGCTCATCTTTGCCTTCCTCC 1078
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      DB 22; Length 993;
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ACAT related gene product 1; human; sterol esterification;
inhibitor; atherosclerosis; hyperlipidaemia; ss.
                                                0; Mismatches 125; Indels
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      Score 95;
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58.78;
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Query Match
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Matches 186; Conservative
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P-PSDB; AAW43406.
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Claim 5; Fig 15A-B; 121pp; English.

The present invention provides human cDNAs, proteins and related genomic DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequence

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was identified following database searching for human ACAT-related sequences and use of PCR and RACE to obtain full-length sequences. To sequences and use of PCR and RACE to obtain full-length sequences. An isolated nucleic acid (see AAV01534) for human ARGP-2 (see AAW43407) was also identified. Also claimed are host vector systems for ARGP-1 and ARGP-2 nucleic acids can be used to diagnose or treat a subject who has an imbalance in sterol levels due to a defect in sterol esterification. A claimed oligonucleotide capable of specifically hybridising to a unique sequence of nucleotides in the isolated nucleic acid molecule, or a vector expressing the oligonucleotide, can be used to inhibit wild-type ARGP-1 or ARGP-2. The Wild-type enzymes can be used to identify an inhibitor, useful in the treatment of atherosclerosis or hyperlipidaemia.
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                                             vrol acyltransferase II (see AAW43406), or ACAT related (
(ARGP-1), that is expressed at high levels in intestine
                          human acylcoenzyme
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                       isolated nucleic acid molecule encodes
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                                               A:cholesterol
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70 ag	901 TITGCCCAGGCCCTGGGANGTGTGCTCTATGCCTGCTTCATCGGGCCGCCTCTGTGTT 960	
Oy 96	961 CCTGTCTTTGCCAACATGAGCCGAAGAGCCCTTCAGCACCCGTGCCGGGGGCTCTCTATC 1020	1
Oy 1021 Db 1072	21 CTGCATGCCACGTGCCAGGCATCTTCATGCTGCTGCTCATCTTTGCCTTCCTCCAT 1080	INFO
Qy 1081 Db 1132	B1 TGCTGGCTCAACGCCTTTGCCGAGATGCTACGATTGCAGACAGGATGTTCTACCGGGAC 1140	; LENGTH: ; TYPE: r ; STRANDEI ; TOPOLOG)
Oy 1141 Db 1192	1141 TGGTGGAACTCAACGTCCTTCCCAACTACTACCGCACTTGGAACGTGGTGGTCCATGAC 1200	
Oy 120	1201 IGGCTGTACAGCTACGTGTATCAGGATGGGCTGGCGCTCTTGGTGCCCGGGCCCGAGGG 1260 	US-08-121-057-: Query Match Best Local S:
Oy 12	1261 GTAGCCATGCTGGGTGTGCTCCGGCTCCGCAGTGCCCATGAGTATATCTTCTGCTTC 1320	Matches 287
Oy 13:	321 GTCCTGGGGTTCTTCTATCCCGTCATGCTGATACTCTTGTCATTGCAGGAATGTTG 1380	347
Oy 13	.381 AACTTCATGATGCATGGCCGGCCGGCATGGAACGTGCTGATGTGGACCATG 1440 	L 4 1
Oy 14 Db 14	1441 CTGTTTCTAGGCCAGGGAATCCAGGTCAGCTGTACTGCCAGGAGTGGTAGGCACGGCGG 1500	Qy 467 TGAT

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1552 CACTGCCCCTACCCCAGGCAACTTTCTGGGGGCTGGTGACACCTCGATCTTGGTCGTGCTTGCT	PRESULT 3 US-08-121-057-3 US-08-121-057-3 US-08-121-057-3 PATENT NO. 5464727 PATENT NO. 5464727 PATENT GRANG, TA-YUAN APPLICANT: GRANG, TA-YUAN APPLICANT: GRANG, CATHERINE C. Y. TITLE OF INVENTION: ACTL TOORNYME A: CHOLESTEROL STREET: BA COUNTRY: USA ZTATE: NA COUNTRY: USA ZTATE: NA COUNTRY: TEM PC COMPATIBLE COMPUTER READBLE FORM: WEDINH TIPE: FLORPY disk COMPUTER READBLE FORM: COMPUTER READBLE FORM: COMPUTER READBLE FORM: COMPUTER READBLE FORM: APPLICATION DAME: COMPUTER TOORNYME ASCILL PACT COMPUTER TOORNYME ASCIL	LAMPON MATION MICE/DOC	Query Match Best Local Similarity 18.9%; Pred. No. 1.16-94; Matches 707; Conservative O. Mismatches 509; Indels 26; G Matches 707; Conservative O. Mismatches 509; Indels 26; G 287 CATCCTGGGGAACAGAAGTTTTCATCTCCCCAGTCCTTCTTGATGGCTGATGG O. Mismatches 509; Indels 26; G 1737 CACCTGGGGAACAGAAGTTTTATTCATCTCCCAGTCTTCTTGATGATGATCTCTTC O. 347 AGGTGGACCTCCGACCATCTATCATCATCGCTGCTCTTTGATGTCTTCTTCTC O. 347 AGGTGGACTTCTCATCATCATCATCATCGCTGCTCTTCTTCTTCATCATCATCATCATCATCATCATCATCA

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                                                                                                                                    TITLE OF INVENTION: ACYL Coenzyme A: Cholesterol Acyltransferase NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS: ADDRESSE: LAHIVE & COCKTELD, LLP STREFT: 28 STATE STREET: 28 STATE STREET: 28 STATE STREET: 28 STATE STREET: ADDRESSE STATE STREET: ADDRESSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/509,187D FILING DATE: 31-JUL-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                GENERAL INFORMATION:
APPLICANT: Chang, Ta-Yuan and Chang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                              Sequence 3, Application US/08509187D Patent No. 5834283
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TELEPHONE: (617)227-7400
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58.9%;
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REGISTRATION NUMBER: 34,8
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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STRANDEDNESS: single
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1397..3046
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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RESULT 3
JS-08-509-187D-3
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                                                                                               2097 TICTAGGITITGGACCAACAIAIGITGGGTTAGCATATACACTGCCACCAGGTTCCCGGT
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Sequence 3, Application US/09121396 Patent No. 5968749 GENERAL INFORMATION:

RESULT 4 US-09-121-396-3

287 CATCCCTGGGGAAACAGAAAGTTTTCATCATCGCAAGTCCCTGCTTGATGAGCTGATGG 346 347 AGGIGCAGCATTICCGCACCATCIACCACATGIICAICGCTGGCCTGIGIGICTICAICA 406 TGTCTTATGCTTTTGGCAAATTTCCTACCGTTGTTTGGACCTGGTGGATCATGTTCCTGT TCAGCACCCTGGCCATCGACTTCATTGATGAGGGCAGGCTGCTGCTGGAGTTTGACCTAC TGATCTTCAGCTTCGGACAGCTGCCATTGGCGCTGGTGACCTGGGTGCCCATGTTTCTGT CCACCCTGTTGGCGCCGTACCAGGCCCTACGGCTGTGGGCCAGGGGCCACCTGGACGCAGG CTACATTTTCAGTTCCCTATTTTCTGTTTCAACATTGGCGCACTGGCTATAGCAAGAGTT CTCATCCGCTGATCCGTTCTCTTCCATGGCTTTCTTTTCATGATCTTCCAGATTGGAG CGACGGGCCTGGGCTGTGCGCTTTTAGCCGCCCACGCCGTGGTGCTCTGCGCGCTGCCGG -----ACGIGGCCGIGGAGCAICAGCICCCGCCGCCGCCTCCCGIT TICTAGGITITIGGACCAACATATGITGTGTTAGCATATACACTGCCACCAGCTTCCCGGT Length 4011; Indels ; 26; TA-YUAN
CATHERINE C. Y.
ACYL COENIYME A: CHOLESTEROL
ACYLTRANSFERASE (ACAT) 0; Mismatches 509; DB 2; .le-94 Score 405.6; NAME: LAMPORT HAWMITTE, ANN.
REGISTRATION NUMBER: 34,858
REFERENCE/DOCKET NUMBER: DCI-033CPDV
TELECOMMUNICATION INFORMATION:
TELEPAN: (617) 227-2700
TELEPAX: (617) 742-414
INFORMATION FOR SEQ ID NO: 3: Pred. No. PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/509,187
FILING DATE: 07/31/95
ATTORNEY/AGENT INFORMATION: CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/121,396 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCLI TAVE COCKFIELD 25.9%; 58.9%; E: LAHIVE & COC 28 STATE STREET LENGTH: 4011 base, pairs TYPE: nucleic acid Best_Local Similarity 58.9 Matches 767; Conservative SEQUENCE CHARACTERISTICS NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: single ZIP: 02109 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy TITLE OF INVENTION: CHANG, CHANG, linear CLASSIFICATION: STREET: 28 STATE: BOSTON STATE: MA USA MOLECULE TYPE: . STRANDEDNESS: TOPOLOGY: 11 FILING DATE ADDRESSEE: COUNTRY: US-09-121-396-3 Query Match 1797 1917 1977 2037 647 2097 689 407 467 527 587 a g ð ò δ g οy q ŏ g ò ò q

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CURRENT APPLICATION DATA:
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G-----CTACCTCTACTTCCTCTTCTGCCCAACACTCATCTACAGGGAGACTTACCCT
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COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
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Pred. No. 1.1e-94;
0; Mismatches 509;
                                                                            959,950
                                                                                                              121,057
                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. SER. NO. 95
FILING DATE: October 14, 11992
APPLICATION NUMBER: U.S. SER. NO. 12
FILING DATE: SEPTEMBER: 10, 1993
ATTORNEY/AGENT INFORMATION:
NAME: LAMPORT HAMMITTE, ANN.
PCT/US93/09704A
                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: DCI-033CP
                    October 12, 1993
                                                                                                                                                                                    REGISTRATION NUMBER: 34,858
                                                                                                                                                                                                                                              TELEPHONE: (617) 227-2700
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 25.9%;
Best Local Similarity 58.9%;
Matches 767; Conservative (
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TYPE: nucleic acid
STRANDEDNESS: single
APPLICATION NUMBER: FILING DATE: Octob
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                                      CLASSIFICATION:
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                                2396 TITITCIAIGIGIACIACATCTITGAAAGGCTITGIGCCCCCCTIGITICGGAATAICAAA
                                                                                                                                                 GAGATGCTACGATTTGGAGACAGGATGTTCTACCGGGACTGGTGGAACTCAACGTCCTTC
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                                                                                 2456 CAGGAGCCCTTCAGCGCTCGTGTTCTGGTCCTATGTTAACTCCATCTTGCCAGGT
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Patent No. 5484727

GENERAL INFORMATION:
APPLICANT: CHANG, TA-YUAN

APPLICANT: CHANG, CATHERINE C. Y.
TITLE OF INVENTION: ACYL COENZYME A: CHOLESTEROL

TITLE OF INVENTION: ACYLTRANSFERSE (ACAT)

NUMBER OF SEQUENCES: 4

CORRESPONDENCE S: CORRESPONDENCE S: CORRESPONDENCE ADDRESSE: LAHIVE & COCKFIELD

STREET: 60 STATE STREET, SUITE 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/121,057
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ATTORNEY/AGENT INFORMATION:
NAME: LAMPORT HAMMITTE, ANN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109
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                                                                                                                                                                                                                                                                                                                                                   22.9%; Score 359.8; DB 1; 58.0%; Pred. No. 6.6e-83; iive 0; Mismatches 502;
REGISTRATION NUMBER: 34,858
REFERENCE/DOCKET NUMBER: DCI-033CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-5700
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 4079 base pairs
                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 58.0 Matches 722; Conservative
                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                  US-08-121-057-2
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1406 CCGCCCCGCCATGGAACGTGCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATCCAGG 1465
 TGCTACGATTTGGAGACAGGATGTTCTACCGGGACTGGTGGAACTCAACGTCCTTCTCCA :1165
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                       ACTACTACCGCACTTGGAACGTGGTGGTCCATGACTGGCTGTACAGCTACGTGTATCAGG 1225
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                                                                                                                                             ATGGGCTGCGGCTCCTTGGTGCCGGGCCCGAGGGTAGCCATCCTGGGTGTGTTCCTGG
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Cholesterol Acyltransferase
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DCI-033cpdv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chang, Ta-Yuan and Chang,
TITLE OF INVENTION: ACYL COENZYME A:
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/509,187D
FILING DATE: 31-JUL-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08509187D Patent No. 5834283 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (617)227-7400
(617)742-4214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 4079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Lamport Hammitte, REGISTRATION NUMBER: 34
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; MOLECULE TYPE: cDNA
US-08-509-187D-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                          21;
  Length 4079;
                           Indels
                        502;
Score 359.8; DB 2
Pred. No. 6.6e-83;
); Mismatches 502
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 22.9%;
58.0%;
                        Conservative
              Similarity,
                        Matches 722;
              Best Local
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                                             1346 TGCTGATACTCTTCCTTGTCATTGGAGGAATGTTGAACTTCATGATGCATGACGAGGGCA
                                                                       2888 IGTICGIGCICIICAIGIICIIIIGGAAIGGCIIIICAACIICAIIGICAAIGAIAGICGGA
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                                                                                                                                                               TCAGCCTGTACTGCCAGGAGTGGTACGCACGGCGGCACTGCCCCT 1510
                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: CHANG, TA-YUAN
APPLICANT: CHANG, CATHERINE C. Y.
TITLE OF INVENTION: ACYL COENZYME A: CHOLESTEROL
TITLE OF INVENTION: ACYLTRANSFERASE (ACAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 359.8; DB 2;
Pred. No. 6.6e-83;
0; Mismatches 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: LAMPORT HAWMITTE, ANN.
REGISTRATION NUMBER: 34,858
REFENCE/DOCKET NUMBER: DCI-033CPDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-2700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/121,396 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/509,187
FILING DATE: 07/31/95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                      5-09-121-396-2
Sequence 2, Application US/09121396
Patent No. 5968749
                                                                                                                                                                                                                                                                                                                                                                                                       2: LAHIVE & COCKFIELD 28 STATE STREET
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TELEFAX: (617) 742-4214
INPCRMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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al Similarity 58.0%;
722; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & C
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CITY: BO
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CITY: BOSTON
STATE: MA
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US-08-121-057-1
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DB 5;
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                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. SER. NO. 959,950
FILING DATE: October 14, 1992
APPLICATION NUMBER: U.S. SER. NO. 121,057
                                                                                                                             ACYL COENZYME A: CHOLI ACYLTRANSFERASE (ACAT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 359.8;
                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US93/09704A
                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: DCI-033CP TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-2700
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                    Sequence 2, Application PC/TUS9309704A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            FILING DATE: September 10, 1993
ATTORNEY/AGENT INFORMATION:
NAME: LAMPORT HAMMITTE, ANN.
REGISTRATION NUMBER: 34,858
                                                                                                                                                                                                                   PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                            October 12, 1993
                                                                                                                                                       NUMBER OF SEQUENCES: 9
COMPUTER READABLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC COMPATIBLE
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58.0%;
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                    COMPUTER: IBM PC COMPOPERATING SYSTEM: PC SOFTWARE: ASCII Text
                                                                                                                             TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                            FILING DATE:
                                                                     PCT-US93-09704A-2
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ACTITICICICGITITICICCAAGAGAITCAAAICIGCIGCCAIGITAGCIGICITIGCIG 2827
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Patent No. 5484727
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CHANG, TA-YUAN
TILLE OF INVENTION: ACYL COENZYME A: CHG;
TITLE OF INVENTION: ACYL COENZYME A: CHC;
TITLE OF INVENTION: ACYLTRANSFERASE (ACK;
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
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us-09-918-026a-3.rni

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862 ATCCCACTGTAAGATGGGGTTATGTTGCTATGAAGTTTGCACAGGGTCTTTGGTTGCTTTT 921
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APPLICANT: Chang, Ta-Yuan and Chang, Catherine C.Y.
TITLE OF INVENTION: ACYL Coenzyme A: Cholesterol Acyltransferase
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                                     TCTATGCCTGCTTCATCCTGGGCCGCCTCTGTGTTCCTGTCTTTGCCAACATGAGCCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: DCI-033cpdv
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/509,187D
FILING DATE: 31-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                     1: LAHIVE & COCKFIELD, LLP
28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                            Sequence 1, Application US/08509187D Patent No. 5834283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lamport Hammitte, Ann RATION NUMBER: 34,858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 996 base pairs
nucleic acid
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                                                                                                                                          982 AGCCCTTCAGCGCTC 996
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CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
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                                                                                                                                                                                                                        RESULT 11
US-08-509-187D-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 134.6;
Pred. No. 2.6
                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,057
FILING DATE:
                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: LAMPORT HAMMITTE, ANN.
REGISTRATION NUMBER: 34,858
REFERENCE/DOCKET NUMBER: DCI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-2700
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ilarity 53.1%;
Conservative
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
                                   COMPUTER READABLE FORM:
                                                                                                                     ASCII Text
                                                                                                                                                                                                     CLASSIFICATION: 800
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US-08-121-057-1
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                            502 TGTCTACATTTTCAGTTCCCTATTTTCTGTTTCAACATTGGCGCACTGGCTATAGCAAGA
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Patent No. 5968749
GENERAL INFORMATION:
APPLICANT: CHANG, TA-YUAN
APPLICANT: CHANG, TA-YUAN
TITLE OF INVENTION: ACYL COENZYME A: CHOLESTEROL
TITLE OF INVENTION: ACYLTRANSFERASE (ACAT)
NUMBER OF SEQUENCES:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/509,187
FILING DATE: 07/31/95
ATTORNEY/AGENT INFORMATION:
NAME: LAMPORT HAWMITTE, ANN.
REGISTRATION NUMBER: 34,858
REFERENCE/DOCKET NUMBER: DCI-033CPDV
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                CCTGTCTTATGCATTTTGGCAAATTTCCTACCGTTGTTTGGACCTGGTGGATGTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            682 TICATCATTATTCGAGCAGATCGTTTTGTAATGAAGGCCCACTCATTTGTCAGAGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 CCAGCTACCTCTACTTCCTCTTCTGCCCAACACTCATCTACAGGGAGACTTACCCTAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 ACCAGTATTTGTACTTCTTATTTGCTCCTACCCTTATCTACCGTGACAGCTATCCCAGGA
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                                                                                                                                                                                            Length ,996;
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                                                                                                                                                                                            Score 134.6; DB 2;
Pred. No. 2.6e-25;
); Mismatches 324;
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                                                                                                                                                                                            8.6%;
ilarity 53.1%;
Conservative
              INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 996 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
(617) 742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCCCTTCAGCACCC 1000
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GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION:
                                                                                                                                                                                                                   Similarity
                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US93-09704A-1
                                                                                                                                                                                                                                       Matches 390;
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                                                                                                                                                                                                Query Match
Best Local
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TITLE OF INVENTION: Acyl-Coa.cholesterol Acyltransferase Related Nucleic TITLE OF INVENTION: Acid Sequences FILE REFERENCE: 17045/00/WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1079 ATTGCTGGCTCAACGCCTTTGCCGAGATGCTACGATTTGGAGACAGGATGTTCTACCGGG 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1019 TCCTGCATGCCACGTTGCCAGGCATCTTCATGCTGCTGCTCTTCTTTTGCCTTCCTCC 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGTAGCCATGCTGGGTGTTCCTGGTCTCCGCAGTGGCCCCATGAGTATATCTTCTGCT 1318
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                                                                                                                                                                    CGCCCTATGTCAGGTGGAATTATGTGGCCAAGAACTTTGCCCAGGCCCTGGGATGTGTGC 925
                                                                                   TCTATGCCTGCTTCATCCTGGGCCGCCTCTGTGTTCCTGTCTTTGCCAACATGAGCCGAG 985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (209)
; OTHER INFORMATION: n at position 209 is unknown
US-09-326-203A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 1999-06-04
CURRENT FILING DATE: 1999-06-04
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/088,143
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/108,389
PRIOR FILING DATE: 1998-11-12
                                                                                                                                                                                                                                                                                                                                                        US-09-326-203A-14
; Sequence 14, Application US/09326203A
; Patent No. 6444876
; GENERAL INFORMATION:
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APPLICANT: Ruezinsky, Diane
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LENGTH: 1895
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Pred. No. 2.6e-25;
0; Mismatches 324;
                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. SER. NO. 959,950
FILING DATE: October 14, 1992
APPLICATION NUMBER: U.S. SER. NO. 121,057
FILING DATE: September 10, 1993
ATTORNEY AGENT INFORMATION:
NAME: LAMPORT HAMMITTE, ANN.
          ACYLTRANSFERASE (ACAT)
                                                                                                                        SOFTWARE: ASCII TAXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US93/09704A
FILING DATE: October 12, 1993
                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: DCI-033CP TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-2700 TELEPAX: (617) 227-5941 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                     34,858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 8.6%;
Best Local Similarity 53.1%;
Matches 390; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 996 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
        TITLE OF INVENTION: AC'
NUMBER OF SEQUENCES: 9
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                              TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL ITLE OF INVENTION: ACYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 95; DB 3; Length 1976;
Pred. No. 5e-15;
0; Mismatches 125; Indels
                                                                                                                                                                                       FILE REFERENCE: 0575/5631
CURRENT APPLICATION NUMBER: US/09/165,042
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
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Job time : 112 secs
                       Sequence 2, Application US/09165042
Patent No. 6100077
                                                                          GENERAL INFORMATION:
APPLICANT: Sturley, Stephen L.
APPLICANT: Oelkers, Peter
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Best Local Similarity 58.7%;
Matches 186; Conservative
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; TYPE: DNA
; ORGANISM: Yeast
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JS-09-165-042-2
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Sequence 14, Appl
Sequence 587, App
Sequence 279, App
Sequence 4564, Ap
Sequence 4664, Ap
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Sequence 33355, A
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                                                                                                                    April 28, 2003, 06:12:58; Search time 113 Seconds
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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10-273-438-9	AENTS SEQUENCES OBTAINED LIBRARIES 995	ch 25.7%; Score 403.6; DB 9; Length 418; 1 Similarity 99.0%; Pred. No. 3.4e-110; 406; Conservative 0; Mismatches 4; Indels 0; Gaps 406; Conservative 0; Mismatches 4; Indels 0; Gaps 4206; Conservative 0; Mismatc
US-09-7-7-10-10-10-10-10-10-10-10-10-10-10-10-10-) 999 008 008 008 008 008 008 008 008 008	;; Score 4 ;; Pred. h 0; Mism 10; Mism 111111111111111111111111111111111111
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249 TGTCATTGGAGGAATGTTGAACTTCATGATGATGACCAGCGCCCGGCCCGGCATGGAA 308
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918, 995
CURRENT APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 33281
LENGTH: 399
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; Sequence 33355, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
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Publication No. US20030073623A1
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Best Local Similarity 100.
Matches 391; Conservative
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US-09-918-995-33281
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROW VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 387.2; DB 9;
Pred. No. 2.5e-105;
0; Mismatches 4;
FROM VARIOUS CDNA LIBRARIES
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PRIOR FILING DATE: 1999-01-20
WUMBER OS DI DNOS: 38054
SOFTWARE: FASTSEO for Windows Version 3.0
                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 33355
                                                       CURRENT APPLICATION NUMBER: US/09/918, 995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
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Publication No. US20030073623A1
GENERAL INFORMATION:
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COTHER INFORMATION: n = A,T,C or
US-09-918-995-33355
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Best Local Similarity 99.0%;
Matches 389; Conservative
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INVENTION:
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LENGTH: 402
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1421

1361

68

1481

Length 402;

DB 9;

24.6%; Score 386;

us-09-918-026a-3.rnpb

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CGTGCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATCCAGGTCAGCCTGTACTGCCA 1481
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 TGTCATTGGAGGAATGTTGAACTTCATGATGCATGACCAGCGCACCGGCCCGGCATGGAA 1421
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                        69 GAACGTGGTGGTCCATGACTGCCTGTACAGCTACGTGTATCAGGATGGGCTGCGGCTCCT
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT APPLICATION NUMBER: US/09/235,076
PRIOR PLILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FREESEQ for Windows Version 3.0
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Pred. No. 2.3e-104;
); Mismatches 0;
                                                                                                                                           GGAGTGGTACGCACGGCGCACTGCCCTTAC 1513
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Publication No. US20030073623A1
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Best Local Similarity 100.0%; Pr
Matches 384; Conservative 0;
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COTHER INFORMATION: n = A,T,C or US-09-918-995-33739
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ORGANISM: Homo sapiens
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LOCATION: (1)...(393)
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                                                      CAGGATGTTCTACCGGGACTGGTGGAACTCAACGTCCTTCTCCAACTACTACCGCACTTG 1181
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                                                                       TGAGTATATCTTCTGCTTCGTCCTGGGGTTCTTCTATCCCGTCATGCTGATACTCTTCCT
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Publication No. US20030073623A1
GENERAL INFORMATION:
TILLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBT
TILLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT FALLATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-207-30
PRIOR FILING DATE: 1999-01-20
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98.7%; Pred. No. 5.8e-105; ive 0; Mismatches 5;
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SOFTWARE: FastSEQ for Windows Version 3.0
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                    Matches 389; Conservative
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US-09-918-995-33843
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LENGTH: 401
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TGTCATTGGAGGAATGTTGAACTTCATGATGCATGACCAGCGCACGGCCCGGCATGGAA 1421
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Publication No. US20030073623A1
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
FITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
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Best Local Similarity 94.9%; Pred. No. 2e-94;
Matches 373; Conservative 0; Mismatches 19;
                                                                                             Score 350.6; DB 9;
Pred. No. 1.9e-94;
0; Mismatches 4;
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                             Query Match 22.3%;
Best Local Similarity 98.9%;
Matches 353; Conservative
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                              sapiens
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                              ; ORGANISM: HOMO & US-09-918-995-34424
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LENGTH: 408
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TILLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
Sequence 33159, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
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Pred. No. 4.8e-102;
0; Mismatches 4;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 34424
LENGTH: 365
                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 33159
LENGTH: 401
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Publication No. US20030073623A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature

LCCATION: (1)...(401)

COTHER INFORMATION: n = A,T,C or G

US-09-918-995-33159
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Best Local Similarity 98.7%;
Matches 389; Conservative
                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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US-09-764-853-79/C
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LENGTH: 993
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US-09-918-995-35056
; Sequence 35056, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; TITLE OF INVENTION NUMBER: US/09/918, 995
; CURRENT APPLICATION NUMBER: US/09/918, 995
; CURRENT FILING DATE: 2001-07-30
; PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FREESE 1999-01-20
; SEQ ID NO 35056
; LENGTH: 383
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Pred. No. 9.7e-91;
0; Mismatches 18;
                                                                                                                                                                    1481 AGGAGTGGTACGCACGCCGCACTGCCCCTTAC 1513
                                                                                                                                                                                                              375 AAGAGTGGGACGCACGGCGCACTGGCCCTTAC 407
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; LCCATION: (1)...(383)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-955-35056
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Best Local Similarity 95.1%;
Matches 349; Conservative
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PUZ06
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 939
SOFTWARE: Patentin Ver. 2.0
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58.7%; Pred. No. 3.6e-18;
iive 0; Mismatches 125; Indels
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                                                                       APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROW VARIOUS CDNA LIBRARIES
FILLE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PADPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTERO for Mindows Version 3.0
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Pred. No. 2.4e-31;
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Sequence 32388, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-32388
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Best Local Similarity 58.79
Matches 186; Conservative
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LOCATION: (1)...(471)
                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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US-09-764-853-79
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Best Local Similarity
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Sequence 14, Application US/10157855 Patent No. US20020170091A1
         956 TCCCTCTGCGAATGTTC 972
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                                                                                                                                          GENERAL INFORMATION:
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ORGANISM: Human
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US-09-764-868-587
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SEQ. ID NO 14
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                                                      1199 ACTGGCTGTACAGCTACGTGTATCAGGATGGGCTGCGGCTCCTTGGTGCCCGGGCCCGAG 1258
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662 recreaageregegerececaareacerearersecrearerretarreraeregerierie 721
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                                                                                         600 AGTGGTGCATCAGACACTTCTACAAGCCCATGCTTCGAC-----GGGGCAGCAGCAAGT
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APPLICANT: Erickson, Sandra
TITLE OF INVENTION: Diacylglycerol O-Acyltransferase
FILE REFERENCE: UCAL-105C1P2
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ilarity 58.7%; Pred. No. 4
Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/273,438
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: US/10/040,315
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/107,771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 10 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2001-10-29
APPLICATION NUMBER: 60/107,771
FILING DATE: 1998-11-09
APPLICATION NUMBER: PCT/US98/17883
FILING DATE: 1998-08-28
APPLICATION NUMBER: 09/103,754
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PRIOR PELING DATE: 1998-11-09
PRIOR PPLING DATE: 1998-08-28
PRIOR APPLICATION UNMBER: 09/103,754
PRIOR APPLICATION UNMBER: 09/339,472
PRIOR APPLICATION NUMBER: 09/339,472
PRIOR FILING DATE: 1999-06-23
                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10273438 Publication No. US20030072757A1 GENERAL INFORMATION: APPLICANT: Farese, Robert V.
                                                                                                                                                                                                          TCGTCCTGGGGTTCTTC 1335
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Matches 186;
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APPLICANT: Ruczinsky, Diane M.
TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic TITLE OF INVENTION: Acid Sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 95; DB 9; Length 189
Pred. No. 4.6e-18;
0; Mismatches 125; Indels
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
                                                                                                                      FILE REFERENCE: 16516.158
CURRENT APPLICATION NUMBER: US/10/157,855
CURRENT FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: 09/326,203
PRIOR FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 60/088,143
                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/108,389
PRIOR FILING DATE: 1998-11-12
NUMBER OF SEQ ID NOS: 46
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Patent No. US20020168711A1
APPLICANT: Lassner, Michael W.
APPLICANT: Ruezinsky, Diane M
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Best Local Similarity 58.7%;
Matches 186; Conservative
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1019 TCCTGCATGCCACGTTGCCAGGCATCTTCATGCTGCTGCTCATCTTTGCCTTCCTCC 1078
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Pred. No. 6.5e-18;
0; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (507)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-868-587
                                                                                                                                                                         LOCATION: (377)

DTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: SITE
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Job time : 130 secs
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Best Local Similarity 58.8%;
Matches 183; Conservative (
NUMBER OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 587
LENGTH: 542
                                                                                        TYPE: DNA ORGANISM: Homo sapiens FEATURE: NAME/KEY: SITE
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AL527439 AL527439 AA867129 vx23f11.r BG696168 602659280

BG500675 602547068 AA867128 vx23f10.r

AI049480 ub37e11.r AU099137 AU099137

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BF681650 602155732 BG698372 602658292

BG105756 602311984 BG743201 602634363 AA410072 EST02151 AW466137 BP230022A

Scoring table:

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Perfect score:

Title:

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Sequence:

BE013288 123187 MA BQ887458 AGENCOURT AA867781 VX16e09.r BE861030 UI-M-API-BQ200762 UI-R-EBI-BF968277 602269663

R10272 yf36b09.r1 BR578775 602094805 A1181841 uh87h09.r AW425878 58867 MAR BB026601 db28h02.x BG105795 60212644 AL773907 AL773907

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602935999F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5099063 5', MI222037
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11238 row: b column: 24
High quality sequence start: 28
High quality sequence story: 798.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc. (
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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BQ200762
BF968277
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AW425878
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BG105795
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BE025829
BQ521546
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BG698372
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BI222037
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DEFINITION
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TITLE
JOURNAL
COMMENT
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KEYWORDS
SOURCE
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BG920709 602814607
BG105735 602311957
BG674469 602620487
BG529751 602560622
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                                                                                                                                    April 28, 2003, 04:51:57; Search time 1603 Seconds (without alignments) 15851.977 Million cell updates/sec
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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BG920709
BG105735
BG674469
BG529751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BI222037
                                                                                                                                                                                                                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 su
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Maximum DB seq length: 200000000
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em_gss_rod:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                em_gss_hum:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                em_gss_pln:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      em_gss_mam:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             em_gss_mus:*
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em_estom:*
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em_htc:*
gb_est1:*
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em_estmu:*
em_estov:*
em_estpl:*
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gb_est3:*
gb_est4:*
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Match Length
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21.4
19.0
17.9
17.4
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BM48569 PGHLC.PkO BE025829 DGHLC.PkO BE025829 DGHC2.y BD621546 NISC_N111 BF130076 601817955 BB877762 BB872762 BJ016863 BJ016863 BJ028057 BJ028057 W7641 Zd67612.rl BJ014628 BJ014628 R07295 yf14e10.rl

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FEATURES

Score

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Result

402.4 335.8 298.2 281.6 272.6

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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904 e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                           1 (bases 1 to 563)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
                                                                                               Ruminantia; Pecora; Bovoidea;
                                                                     Euteleostomi;
                                                                                                                                                                               Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Lagreid, W.W., Chirer, G.A., Chitko-McKown, C.C. Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sall;
                                                                                                                                                                                                                                                                                         normalized bovine cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAAACGCGGAGGTGCACAGAGGCCCAGATTTGGTGCAATGGACCCAGCATATGCAGGCT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2:
Library made from pooled tissue from day 20 and da
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Length 563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                 Sequence evaluation of four pooled-tissue normalized b
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
                                                                   Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63; Indels
                                                                                                                                                                                                                                                                                                                                                                                   Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
T=1: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 335.8; DB 1
Pred. No. 5.9e-68;
0; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 t
                                                Bos taurus
Eukaryota; Metazoa; Chordata; Craniat
Mammalia; Eutheria; Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 4BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plate: 55 row: 0 column: 15 Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACKWARD: GITITCCCAGICACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 g
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                                                                                                                         Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 21.4%;
Best Local Similarity 85.6%;
Matches 373; Conservative
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160 c
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KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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AUTHORS
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                       /organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="InAGE:5099063"
/clone="InAGE:5099063"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: liver; Vector: pCMMV-SPORT6; Site_1: Not1;
/note="Organ: liver; Vector: pCMMV-SPORT6; Site_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     612 AGCCGCCCACGCCGTGGTGCTCTGCGCGCTGCCGGTCCACGTGGCCGTGGAGCATCAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324 GICCCIGCTIGAIGAGCIGAIGGAGGIGCAGCATITCCGCACCAICTACCACAIGTICAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACCTGGGTGCCCATGTTTCTGTCCACCCTGTTGGCGCCCGTACCAGGCCCTACGGCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       673 GOCCAGGCGGCGCGGGGGGGGCCTGGATGCTGGGGGGCCAGCCTGGGCTGCGTACTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       444 GCTGCTGCTGGAGTTTGACCTACTGATCTTCAGCTTCGGACAGCTGCCATTGGCGCTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                               Score 402.4; DB 13; Length 799;
Pred. No. 1.8e-83;
0; Mismatches 126; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE236762 563 bp mRNA linear L4578 MARC 4BOV Bos taurus cDNA 5', mRNA sequence. BE236762.1 GI:9021480
                                                                                                                                                                                                                                                                                                                                                    Query Match 25.6%;
Best Local Similarity 78.7%;
Matches 524; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          672 CCCGCC 677
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BE236762
LOCUS
DEFINITION
ACCESSION
VERSION
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: gapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMN10912 row: n column: 01
High quality sequence start: 15
High quality sequence start: 15
High quality sequence stop: 778.
L. 778
Location/Qualifiers
L. 778
//straine*FVB/N"
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 778)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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488 AGGCTGATGATGGANTTCGATCTACTGACCTTCACCTTCGGACAGCTGCCCTTGGCTCTG 547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                  mRNA sequence.
BG920709
BG920709.1 GI:14301185
                                  Mus musculus
                                                                                                                                                                                                                                                                             house mouse.
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JOURNAL
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/clone_lib="NIH_MGC_84"
/clone_lib="NIH_MGC_84"
/clone_lib="NIH_MGC_84"
/clone_lib="NIH_MGC_84"
/tlssue_type="adrenal cortex carcinoma, cell line"
/lab.host="DH108 (phage-resistant)"
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_l:
NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT
primed. Average insert size 1.229 kb. Library enriched for
full:length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Tissue procurement: ATC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10161 row: a column: 15
High quality sequence stop: 694.
Location/Qualifiers
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//organism="Homo sapiens"
//db.xref="taxon:goof"
//db.xref="taxon:goof"
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1 (bases 1 to 705)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                             GACCAGC-GCACCGGCCCGGCATGGAACGTGCTGATGTGGACCATGCTGTTTCTAGGCCA 1454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATCCCGTCATGCTGATACTCTTCCTTGTCATTGGAGGAATGTTGAACTTCATGATGCAT 1395
CCAGGCATCTTCATGCTGCTGCTCATCTTTTGCCTTCCTCCATTGCTGGCTCAACGCC 1095
                                                                                                                                TITGCCGAGATGCTACGATTTGGAGACAGGATGTTCTACCGGGACTGGTGGAACTCAACG 1155
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BG105735
                                         CCAGGTGTCTTGATACTGTTCCTTTCGTTCTTTTGCCTTTTTTGCACTGCTGGCTCAATGCC 350
                                                                                                                                                                   471 GITTACAAAGACCIGCICIGGITITICICGAAGAGGITCAAAICIGCCGCCAIGCIGGCC 530
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 992)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                 Gaps
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                                                               ;
                                       Length
                                                                 Indels
                                      DB 12;
                                                               0; Mismatches 244;
                                     Score 281.6; DB 1 Pred. No. 3.1e-55;
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                                     17.9%;
64.2%;
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                                                              Matches 439; Conservative
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone=lib="NcI_CGAP_Skn3"
/clone=lib="NcI_CGAP_Skn3"
/lab_host="hots" fir j phage resistant)"
/lab_host="hots" skin, Vector: poWV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
216 c 231 g 346 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421
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                       CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) Disquencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10593 row: n column: 22
High quality sequence stop: 828.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1141. TGGTGGAACTCAACGTCCTTCTCCAACTACTACCGCACTTGGAACGTGGTGGTCCATGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 272.6; DB 12;
Pred. No. 4.6e-53;
0; Mismatches 244;
Tissue Procurement: James Cleaver,
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/organism="Homo
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Matches 419; Conservative
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TITLE
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/tissue_type="embryonal carcinoma"
/lab_host="While MGG_61"
/lab_host="While MGG_61"
/lab_host="While MGG_61"
/note="Organ: testis; Vector: pDNR-LIB (clontech); Site_1:
Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc);
Dobble-stranded cDNA was prepared from cell line RNA. 5;
and 3' adaptors were used in cloning as follows: 5;
adaptor sequence: 5'-CACGGCCATATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGGGGCGCATG-GT(30)BN-3'
(where B = A, C, or G and N = A, C, G, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR: This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library.
                                                                                                    BG529751 840 bp mRNA linear EST 03-APR-2001 602560622F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4698748 5', .
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutherita; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 840)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           811 TACCTCTACTTCCTCTTCTGCCCAACACTCATCTACAGGGAGACTTACCCTAGGACGCCC 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGTACTACATCTTTGAAAGGCTTTGTGCCCCCTTGTTTCGGAATATCAAACAGGAGCCC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 268; DB 12; Length 840;
Pred. No. 5.1e-52;
0; Mismatches 260; Indels .6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 TATTIGIACTICITATTIGCICCTACCCTTAICTACCGIGACAGCTATCCCAGGAATCCC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCTGCTTCATCCTGGGCCGCCTCTGTGTTCCTGTCTTTGCCAACATGAGCCGAGAGCCC
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High quality sequence stop: 764.
Location/Qualifiers
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/clone="IMAGE:4698748"
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                                                                                                                                          mRNA sequence.
BG529751
BG529751.1 GI:13521288
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Best Local Similarity 63.4%;
Matches 460; Conservative
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Best Local Similarity
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CGT 664
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ORIGIN
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AUTHORS ·
TITLE
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COMMENT
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                                                           RESULT 6
BG529751
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/tissue_type="neuroblastoma cells"
/lab.host="DH10B"
/note="Corgan: brain, Vector: pCMVSPORT 6; 1st strand cDNA was primed with a Not!-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and coloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
Unpublished (2001)
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1051 CTGCTGCTCA-TCTTCTTTGCCTTCCTCCATTGCTGGCTCAACGCCTTTGCCGAGATGCT 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1350 GATACTCTTCCTTGTCATTGGAGGAATGTTGAACTTCATGATGCATGACCAGCGCAC-CG 1408
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr.
Location/Qualifiers
                                                                                                                                                                                                                                        1170 CTACCGCACTTGGAACGTGGTGGTCCATGACTGGCTGTACGTGTACGTATCAGGATGG
                                                                                                                                                   1110 ACGATTTGGAGACAGGATGTTCTACCGGGACTGGTGGAACTCAACGTCCTTCTCCAACTA
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                                                        252 CTCTTCCTTACTTTTTTTTGCCTTTTTGCACTGCTGGCTCAATGCCTTTGCTGAGATGTT
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/db_xref="taxon:9606"
/clone="cS0Dc021YJ22"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
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 of Invitrogen 9800 Medical Center
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 Technologies, a division of Invitrogen 9800 Medical cen Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filangelifetech.com URL : http://fullength.invitrogen.com"
a 207 c 1885 g 308 t 8 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GATGAAGGAAGCTGGTGCTTGAGTTCAGCCTCCTGTCTTATGCTTTTGGCAAATTTCCT
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                                                                                                                                                                                                                                                                                                                                                                                          241 GTGTTAGCATATACACTGCCACCAGCTTCCGGTTCATCATTATATTTGAGCAGATTGGT
                                                                                                                                                                                                           193 TIGGGGGCIGGTGACCIGGGIGCCCAIGITICIGICCACCCIGITGGCGCCGIACCAGGCC
                                                                                                                                                                                                                                                                CTACGGCTGTGGGCCAGGGGCACCTGGACGCGACGGGCCTGGGCCTGTGCCCTTTTA
                                                                                                                                                                                                                                                                                                                                               181 CATGGCTTTCTTTCATGATCTTCCAGATTGGAGTTCTAGGTTTTGGACCAACATATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     775 CGAGGTGAGGGGATCCAGGCCCCCAGTTTCTCCAG-----CTACCTCTACTTCCTCTT
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                                                                                                                           26;
                                                                                            Score 264; DB 9; Length 893;
Pred. No. 4.5e-51;
6; Mismatches 341; Indels
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ilarity 58.3%;
Conservative
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                                                                                                   Query Match
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RESULT 8

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Marram, Hillier, Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA
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AA867129 694 bp mRNA linear EST 16-MAR-19 vx23f11-r1 Soares_thymus_to 9b:L42293 Mus musculus cohA clone IMAGE:1265325 5' similar to 9b:L42293 Mus musculus acyl-coenzyme A:cholesterol acyltransferase (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      through LLNL; contact the ') for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 CCTTTCGTTCTTGCCTTTTTGCACTGCTGGCTCAATGCCTTTGCTGAGATGTTACGCTT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                936 CTTCATCCTGGGCCGCCTCTGTGTTCCTGTCTTTGCCAACATGAGCCGAGAGCCCTTCAG 995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free throug
IMAGE Consortium (info@lmage.llnl.gov) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.7%; Score 246.2; DB 9; 63.4%; Pred. No. 5.9e-47; iive 0; Mismatches 218;
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/clone_lib="Soares_thymus_2NbMT"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primer: -28ml3 rev2 ET from Amersham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 441.
Location/Qualifiers
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/db_xref="taxon:10090"
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/dev_stage="4 weeks"
/lab_host="DH10B"
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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902 TTGCCCAGGCCCTGGGATGTGTGCTCTATGCCTGCTTCATCCTGGGCCGCCTCTGTGTTC 961
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-rémail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLAM10696 row: p column: 20
High quality sequence start: 5
High quality sequence stop: 738.
Location/Qualifiers
                                                                                                 1295
                                         CACTTGGAACGTGGTGGTCCATGACTGCTGTACACGTGTGTATCAGGATGGGCTGCG 1235
                                                                                                                                                         1296 GGCCCATGAGTATATCTTCTGCTTCGTCCTGGGGTTCTTCTATCCCGTCATGCTGATACT 1355
                                                                                                                                                                                                                                                                       1416 ATGGAACGTGCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATCCAGGTCAGCCTGTA 1475
                                                                                                                                                                                                               1356 CTTCCTTGTCATTGGAGGAATGTTGAACTTCATGATGCATGACCAGCGCACCGGCCCGGC 1415
                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 741)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                      421
182 TGGTGACAGGATGTTTTATAAGGACTGGTGGAACTCTACATCATACTCCAACTACAACACA 241
                                                                                                                                                                                                                                            481
                                                                      242 GACCTGGAACGTGGTGCACGACTGGCTCTACTACTATGTTTACAAAGACCTGCTCTG 301
                                                                                                                                                                                                                                                                                                  482 CTCGAACATCACGGTTTGGGCTTCTCTTGTTCCTGGGCTATGGACTCATTCTGTGCTTTTA 541
                                                                                                                                                                        1236 GETCCTTGGTGCCCGGGCCCGAGGGTAGCCATGCTGGGTGTGTTCCTGGTCTCCGCAGT
                                                                                                                                                                                                                                            CTTCATGTTCTTTGGAATGGCTTTTTAACTTCATTGTTAACGACAGTCGGAAAAGGCCAAT
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Best Local Similarity 63.9%; Pred. No. 1.2e-46;
Matches 402; Conservative 0; Mismatches 225; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 741 bp 602659280F1 NCI_CGAP_Skn3 Homo s
                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
BG696168
BG696168.1 GI:13961039
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Gaps

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ub37ell.rl Soares_thymus_2NbMT Mus musculus cDNA clone
IMAGE:1379944 5' similar to 9b:L21934 STPROL O-ACYLTRANSFERASE
(HUMAN); 9b:L4293 Mus musculus acyl-coenzyme A:cholesterol
acyltransferase (MOUSE);, mRNA sequence.
A1049480.1 GI:3297767
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                GGCTGTACAGCTACGTGTATCAGGATGGGCTGCGGCTCCTTGGTGCCCGGGCCCGAGGGG 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1262 TAGCCATGCTGGGTGTTCCTGGTCTCCGCAGTGGCCCATGAGTATATCTTCTGCTTCG 1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1322 TCCTGGGGTTCTTCTATCCCGTCATGCTGATACTCTTCCTTGTCATTGGAGGAATGTTGA 1381
                                                                          CTGTCTTTGCCAACATGAGCCGAGAGCCCTTCAGCACCCGTGCCCTGGTGCTCTCTATCC 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTGGAACTCCACGTCATACTCCAACTATATATAGAACCTGGAATGTGGTGGTCGTGACTTGACT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCCATGTTAGCTGTCTTTGCTGTATATCTGCTGTAGTACACGAATATGCCTTGGCTGTTT 430
                                                                                                         CCTTGTTTCGGAATATCAAACAGGAGCCCTTCAGCGCCCTGGTTCTGGTCTTGTGTTAT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTGGAACTCAACGTCCTTCTCCAACTACTACCGCACTTGGAACGTGGTGGTCCATGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTTTCTAGGCCAGGGAATCCAGGTCAGCCTGTACTGCCAGGAGTGGTACGCACGGCGGC
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
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The WashU-HHMI Mouse EST Project
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ATTCTCAAGAGTGGTATGCCCGCCAGCACTGTCCTCTGAAGAACCTACATTTCTGG 605
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                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:902416 Seq primer: -28ml3 rev2 ET from Amersham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     996 CACCCGTGCCCTGGTGCTCTTATCCTGCATGCCACGTTGCCAGGCATCTTCATGCTGCT 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1116 TGGAGACAGGATGTTCTACCGGGACTGGTGGAACTCCAACGTCCTTCTCCCAACTACTACCG 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1236 GCTCCTTGGTGCCCGGGCCCGAGGGGTAGCCATGCTGGGTGTGTTCCTGGTCTCCGCAGT 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1296 GGCCCATGAGTATATCTTCTGCTTCGTCCTGGGGTTCTTCTATCCCGTCATGCTGATACT 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1356 CTTCCTTGTCATTGGAGGAATGTTGAACTTCATGATGCATGACCAGC-GCACCGGCCCGG 1414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1415 CATGGAACGTGCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATCCAGGTCAGCCTGT 1474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 CTACATCTTTGAGAGACTCTGTGCCCCACTATTCCGGAATATCAAACAGGAGCCCTTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 TGGTGACAGGATGTTTTATAAGGACTGGTGGAACTCTACATCATACTCCAACTACTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 GACCTGGAACGTGGTGGTGCACGACTGCTTCTACTATGTTTACAAAGACCTGCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310 GITITICICGAAGAGGITCAAAICIGCCGCCAIGCTGGCCGCTGTICGCCCTGTCGGCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Pred. No. 7.2e-46;
0; Mismatches 214;
                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="IMAGE:1379948"
/clone_lib="Soares_thymus_2nbwT"
/sex="male"
                                                                                                                                             1. .731
/organism="Mus musculus"
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                        High quality sequence stop: 313.
Location/Qualifiers
                                                                                                                                                                                  /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 15.4%;
Best Local Similarity 63.9%;
Matches 381; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 300)
Suzukl,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
In silico mapping of the 5'-ends of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries constructed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched CDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
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linear | EST 05-APR-2001
AU099137 AU099137 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HEP20912 similar to Homo sapiens acyl coenzyme A:cholesterol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethyliumarate treated U937 cells"
79 c 108 g 35 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GAGCGCCAACCCTGTGGAGATGGAAACACTGAGACGCACAGAGCCCCGGACTTGGTACAA
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O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedal, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 300;
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1.1e-45;
0;
                                                                        acyltransferase 2 mRNA, mRNA sequence.
AU099137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP20912"
                                                                                                                               AU099137.1 GI:13550266
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                                                                                                                                                                                                                                                                                                                                                                                                                               Oligo-capping method Unpublished (2001)
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//do_aracan:9606"
//do_aracan:9606"
//clone="IMAGE:4669480"
//clone="Image:4608"
//clone=lib="NIH_MGC_60"
//clone=lib="NIH_MGC_60"
//lab_host="DH10B (TI phage=resistant)"
//note="Organ: prostate; Vector: pDNR-LIB (Clontech);
//note="Organ: pp organization org
                                Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     988 CCCTTCAGCACCCGTGCCCTGGTGCTCTTATCCTG-CATGCCACGTTGCCAGGCATCTT 1046
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                   Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostom Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 846)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 811 TACCTCTACTTCCTCTTCTGCCCAACACTCATCTACAGGGAGACTTACCCTAGGACGCCC 870
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                                                                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/TLNL at:
http://image.llnl.gov
Plate: LLCM1481 row: g column: 17
High quality sequence stop: 684.
Location/Qualifiers
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63.2%; Pred. No. 3.5e-45;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Musi. I (Dases 1 to 887)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                CCGCCCCGGCATGGAACGTGCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATCCAGG 1465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
1227 regecrecescrectregrecesesecesasserasecrasserseseseseser
                                                                                                     CTCCGCAGTGGCCCATGAGTATATCTTCTGCTTCGTCCTGGGGTTCTTCTATCCCGTCAT 1346
                                                                                                                                                                                                           GCTGATACTCTTCCTTGTCATTGGAGGAATGTTGAACTTCATGATGCATGACCAGC-GCA 1405
                                                                                                                                                                                                                                                            553 CTTCGTGCTCTTCATGTTCTTTGGAATGGCTTTCAACTTCATTGTCAATGATAGTCGGAA 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA867128 B87 bp mRNA linear EST 16-MAR-vx23f10.rl Scares_thymus_2NbMT hus musculus cDNA clone IMAGE:1265323 5, similar to gb:L21934 STEROL O-ACYLTRANSFERASE (HUMAN); gb:L42293 hus musculus acyl-coenzyme A:cholesterol acyltransferase (MOUSE);, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                     613 AAAGCCCGATCTGGAATGTTCTGATGTGGACTTCTCTTTTCTTGGGCAATGGAGTCTTAC 672
                                                                                                                                 CTITCICIGETITICICCAAGAGATICAGATCIGCCGCCAIGTIAGCTGCTTTGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1265323"
/clone_lib="Soares_thymus_2NbMT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: -28m13 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 447 Location/Qualifiers
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/dev_stage="4 weeks"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1996)
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Fax: 314 286 1810
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Pan troglodytes
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 Library went through two
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Pan troglodytes DNA, clone: PTB-145020.F, genomic survey sequence:
AG133295
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Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1364
                                                                                                                                                                                                                                                                   1065 CTTTGCCTTCCTCCATTGCTGGCTCAACGCCTTTGCAGATGCTACGATTTGGAGACAG 1124
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                 constructed by Bento
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                                                                                                                   887;
                                                                                                             Score 233.8; DB 9; Length
Pred. No. 5.2e-44;
0; Mismatches 197; Indels
provided by Dr. Bertrand Jordan. rounds of normalization, and was Soares and M.Fatima Bonaldo."
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BAC end sequences of Library PTB
Unpublished
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                                                                                                               Query Match 14.9%;
Best Local Similarity 64.1%;
Matches 352; Conservative
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1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mall:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D.process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG697784 1inear EST 07-MAY-2001 602661272F1 NCI_CGAP_SKn3 Homo sapiens CDNA clone IMAGE:4804481 5',
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Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               899
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 635;
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217 c 189 g 126 t
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Pred. No. 1.3e-42;
0; Mismatches 14;
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                                                                                                                                                                                                                                                                                  /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                         /sex="male"
/cell_type="lymphoblast"
                                                                                                                                                                                                                                                                                                                       /clone="PTB-145020.F"
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                                                                                                               clone tracking errors.
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Best Local Similarity 90.6%;
Matches 259; Conservative
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Mammalia; Eutheria;
1 (bases 1 to 848)
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BG697784
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http://image.llnl.gov
Plate: LiAMIO701 row: p column: 18
High quality sequence stop: 808.
Location/Qualifaers
1. 848
//organism="Romo sapiens"
//db_xref="taxon:9606"
//clone="lkAGE:4804481"
//lab_host="bH108 (T1 phage-resistant)"
//lab_host="bH108 (T1 phage-resistant)"
//note="Organ: skli; Vector: pCMV-SPORT6; Site_1: NotI;
//note="Organ: skli; Vector: pCMV-SPORT6
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Search completed: April 28, 2003, 08:57:41 Job time : 1630 secs

(OTAZU) NNAJA 32A9 ZIHT